GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 22, 2002, 15:46:32 ; Search time 22.6 Seconds
(without alignments)
114.728 Million cell updates/sec

Title: US-09-534-376A-5
Perfect score: 87
Sequence: 1 XEEIIKFAAAHYNIEILK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174506 seqs, 146272429 residues

Total number of hits satisfying chosen parameters: 4213

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	87.4	420	6	Q9XS50	Q9XS50 Bos taurus
2	69	79.3	418	13	O57352	O57352 Coturnix co
3	42.5	48.9	463	4	Q9NVT8	Q9NVT8 Homo sapien
4	42.5	48.9	463	4	Q9B9J7	Q9B9J7 Homo sapien
5	42.5	48.9	664	4	Q9H455	Q9H455 Homo sapien
6	42	48.3	389	2	Q9X4V0	Q9X4V0 Streptococc
7	42	48.3	406	2	O51494	O51494 Borrelia bu
8	42	48.3	558	2	Q9FBN4	Q9FBN4 Streptomyce
9	42	48.3	1058	13	Q91480	Q91480 Salmo salar
10	42	48.3	1187	13	Q98TF0	Q98TF0 Cyprinus ca
11	42	48.3	4307	5	Q19419	Q19419 Caenorhabdi
12	41	47.1	98	10	Q9ARH0	Q9ARH0 Dianthus ca
13	41	47.1	233	1	Q9YDH4	Q9YDH4 Aeropyrum p
14	41	47.1	426	11	O35251	O35251 Rattus norv
15	41	47.1	458	11	P97946	P97946 Mus musculu
16	41	47.1	836	5	O17118	O17118 Caenorhabdi
17	40.5	46.6	100	2	O87301	O87301 Borrelia bu
18	40.5	46.6	174	2	Q9LVM8	Q9LVM8 Borrelia bu
19	40.5	46.6	179	2	Q9S039	Q9S039 Borrelia bu
20	40	46.0	98	10	Q9ZIB4	Q9ZIB4 Dianthus ca
21	40	46.0	238	9	Q838Q1	Q838Q1 Lactococcus
22	40	46.0	352	2	Q9CC65	Q9CC65 Mycobacteri
23	40	46.0	368	2	Q49622	Q49622 Mycobacteri
24	40	46.0	765	1	Q59019	Q59019 Methanococc
25	39	44.8	108	13	Q90464	Q90464 Brachydanio
26	39	44.8	234	10	Q9CAS6	Q9CAS6 Arabidopsis
27	39	44.8	299	2	Q9XJK4	Q9XJK4 Streptococc
28	39	44.8	317	2	Q9WZX3	Q9WZX3 Thermotoga
29	39	44.8	429	12	Q65258	Q65258 African swi
30	39	44.8	485	2	Q9WXP2	Q9WXP2 Thermotoga
31	39	44.8	965	3	O74762	O74762 Schizosacch
32	39	44.8	1286	4	Q9P2C3	Q9P2C3 Homo sapien
33	38	43.7	209	14	P79929	P79929 Xenopus lae
34	38	43.7	214	13	O42134	O42134 Gallus gall
35	38	43.7	278	10	Q43525	Q43525 Lycopersico
36	38	43.7	329	10	Q9LZG5	Q9LZG5 Arabidopsis
37	38	43.7	332	1	O29922	O29922 Archaeoglob
38	38	43.7	339	2	Q9S1P6	Q9S1P6 Streptomyce
39	38	43.7	447	1	Q9HHA1	Q9HHA1 Methanosarc
40	38	43.7	470	2	Q9ZGE2	Q9ZGE2 Helicobacte
41	38	43.7	517	5	Q9V7M9	Q9V7M9 Drosophila
42	38	43.7	803	5	Q22443	Q22443 Caenorhabdi
43	38	43.7	861	2	Q9X8M7	Q9X8M7 Streptomyce
44	38	43.7	1060	10	O04709	O04709 Zea mays (m
45	38	43.7	1196	13	Q98IE1	Q98IE1 Cyprinus ca

ALIGNMENTS

RESULT 1
Q9XS50
ID Q9XS50 PRELIMINARY; PRT; 420 AA.
AC Q9XS50;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Liu X., Yonekura H., Yamamishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB004275; BAA77687.1; -.
DR HSSP; P15692; 1VPF.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR Prodom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 420 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ SEQUENCE 420 AA, 46681 MW, 58BA863173A3C8E2D CRC64;

Query Match 87.4%; Score 76; DB 6; Length 420;
Best Local Similarity 87.5%; Pred. No. 5e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIIKFAAAHYNIEILK 18
|:||||||||||||||:|
Db 106 EILKFAAAHYNIEILR 121

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RESULT   2
O57452
ID   O57452       PRELIMINARY;      PRT:   418 AA.
AC   O57452;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN   VEGF C.
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=9094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98162988; PubMed=9435264;
RA   Eichmann A., Corbel C., Jaffredo T., Breant V., Joubin V., Kumar V.,
RA   Altiado K., Le Douarin N.M.;
RT   "Avian VEGF C: cDNA, embryonic expression pattern and stimulation
RT   of the differentiation of VEGFR2 expressing endothelial cell
RT   precursors.";
RL   Development 125:743-752(1998).
DR   EMBL; Y10833; CAA71799.1;  -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR002430; GF_cysknot.
DR   InterPro; IPR000476; Glyco_hormone.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GPCYSKNOT.
DR   Prodom; PD001629; PDGF; 1.
DR   SMART; SM00067; GHA; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Signal.
FT   SIGNAL        1     41       POTENTIAL.
FT   CHAIN       111    418       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ   SEQUENCE   418 AA;  46839 MW;  0F9BF0C791C1BF2B CRC64;


  Query Match             29.6%;  Score 69;  DB 13;  Length 418;
  Best Local Similarity   70.6%;  Prod. No. 0.00081;
  Matches   12;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 EEITKFAAAHYNIEILK 18
           ::::|||||||| ||||
Db     104 EDGSEKPAAAHYNAEILK 121


RESULT   3
Q9NVI8
ID   Q9NVI8       PRELIMINARY;      PRT:   463 AA.
AC   Q9NVI8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   cDNA FLJ10514 FIS, CLONE NT2RP2000719, WEAKLY SIMILAR TO ASPARTYL-TRNA
DE   SYNTHETASE (EC 6.1.1.12).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takeuchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + tRNA(AMINO ACID) = AMP +
CC       PYROPHOSPHATE + L-AMINOACYL-tRNA(AMINO ACID).
CC   -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC       tRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-tRNA(ASP) (OR L-
CC       ASPARAGINYL-tRNA(ASN)).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO AMINOACYL-TRANSFER RNA SYNTHETASES CLASS II
CC       FAMILY.
CC   -!- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR   EMBL; AK001376; BAA91658.1;  -.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   InterPro; IPR002309; tRNA_synt_2.
DR   InterPro; IPR002312; tRNA_synt_asp.
DR   InterPro; IPR002313; tRNA_synt_lys_2.
DR   Pfam; PF00152; tRNA_synt_2; 1.
DR   PRINTS; PR01042; TRNASYNTHASP.
DR   PRINTS; PR00982; TRNASYNTHLYS.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
KW   ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ   SEQUENCE   463 AA;  52552 MW;  6536F9644E7F831F CRC64;


  Query Match             48.9%;  Score 42.5;  DB 4;  Length 463;
  Best Local Similarity   62.5%;  Prod. No. 35;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       5 EITKFAAAHYNIEILK 17
           |:|: ||| |:| |||
Db     203 ESIKNFAADHFNQEIL 218


RESULT   4
Q9H9J7
ID   Q9H9J7       PRELIMINARY;      PRT:   463 AA.
AC   Q9H9J7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CDNA FLJ12692 FIS, CLONE NT2RM4002623, WEAKLY SIMILAR TO ASPARTYL-TRNA
DE   SYNTHETASE (EC 6.1.1.12).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takeuchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + tRNA(AMINO ACID) = AMP +
CC       PYROPHOSPHATE + L-AMINOACYL-tRNA(AMINO ACID).
CC   -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC       tRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-tRNA(ASP) (OR L-
CC       ASPARAGINYL-tRNA(ASN)).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO AMINOACYL-TRANSFER RNA SYNTHETASES CLASS II
CC       FAMILY.
CC   -!- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR   EMBL; AK022754; BAB14228.1;  -.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   InterPro; IPR002309; tRNA_synt_2.
DR   InterPro; IPR002312; tRNA_synt_asp.
DR   InterPro; IPR002313; tRNA_synt_lys_2.
DR   Pfam; PF00152; tRNA_synt_2; 1.
DR   PRINTS; PR01042; TRNASYNTHASP.
DR   PRINTS; PR00982; TRNASYNTHLYS.
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DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
KW   ATP binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ   SEQUENCE   463 AA;  52639 MW;  2CA395151402DF9F CRC64;


  Query Match             48.9%;  Score 42.5;  DB 4;  Length 463;
  Best Local Similarity   62.5%;  Pred. No. 45;
  Matches   10;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       3 EIIK-FAAAHYNIEIL 17
           ||| | |||| |||
Db     208 ESIRNFAADHFNQEIL 218


RESULT   5
Q9H455
ID   Q9H455      PRELIMINARY;      PRT:   664 AA.
AC   Q9H455;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Dj383J4.4 (A NOVEL PROTEIN SIMILAR TO ASPARTYL-tRNA SYNTHETASE)
DE   (FRAGMENT).
GN   Dj383J4.4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frankland J.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + tRNA(AMINO ACID) = AMP +
CC       PYROPHOSPHATE + L-AMINOACYL-tRNA(AMINO ACID).
CC   -!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC       tRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL tRNA(ASN) ( OR L-
CC       ASPARAGINYL-tRNA(ASN)).
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO AMINOACYL-TRANSFER RNA SYNTHETASES CLASS II
CC       FAMILY.
CC   -!- SIMILARITY: BELONGS TO ASPARTYL-tRNA SYNTHETASE FAMILY.
DR   EMBL; AL109921; CAC10472.1; -.
DR   InterPro; IPR002106; AA_tRNA_ligase_II.
DR   InterPro; IPR002309; tRNA_synt_2.
DR   InterPro; IPR002312; tRNA-synt_asp.
DR   InterPro; IPR002413; tRNA-synt_lys_2.
DR   Pfam; PF00152; tRNA-synt_2; 1.
DR   Pfam; PF01336; tRNA_anti; 1.
DR   PRINTS; PR01042; TRNASYNTHASP.
DR   TIGRIS; PR00982; TRNASYNTHLYS.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
KW   ATP binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
FT   NON_TER       1       1
SQ   SEQUENCE   664 AA;  75479 MW;  1CAE4D6376D7810A CRC64;


  Query Match             48.9%;  Score 42.5;  DB 4;  Length 664;
  Best Local Similarity   62.5%;  Pred. No. 62;
  Matches   10;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       3 EIIK-FAAAHYNIEIL 17
           ||| | |||| |||
Db     494 ESIRNFAADHFNQEIL 504


RESULT   6
Q9X4V0
ID   Q9X4V0      PRELIMINARY;      PRT:   389 AA.
AC   Q9X4V0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   CPS2F.
GN   CPS2F.
OS   Streptococcus suis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1307;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN 10;
RX   MEDLINE=99184998; PubMed=10085014;
RA   Smith H.E., Damman M., Van der Velde J., Wagenaar F., Wisselink H.J.,
RA   Stockhofe-Zurwieden N., Smits M.A.;
RT   "Identification and characterization of the cps locus of Streptococcus
RT   suis serotype 2: the capsule protects against phagocytosis and is an
RT   important virulence factor.";
RL   Infect. Immun. 67:1750-1756(1999).
DR   EMBL; AF118389; AAD24452.1; -.
SQ   SEQUENCE   389 AA;  45498 MW;  F0F2D372D56138CA CRC64;


  Query Match             48.9%;  Score 42;  DB 2;  Length 389;
  Best Local Similarity   47.1%;  Pred. No. 86;
  Matches    8;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           :: |||    | |:|||
Db     272 PERIEFVGIVYNQEILK 288


RESULT   7
O51494
ID   O51494      PRELIMINARY;      PRT:   406 AA.
AC   O51494;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE (PRS).
GN   BB0544.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN ATCC 35210 / B31;
RX   MEDLINE=98065943; PubMed=9404885;
RA   Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA   Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA   Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA   Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA   van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA   Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA   Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA   Smith H.O., Venter J.C.;
RT   "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT   burgdorferi.";
RL   Nature 390:580-586(1997).
DR   EMBL; AE001156; AAC66912.1; -.
DR   HSSP; P14193; 1UKK.
DR   TIGR; BB0544; -.
DR   InterPro; IPR000836; Pribosyltran.
DR   Pfam; PF00156; Pribosyltran; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   406 AA;  45749 MW;  01F34388FA6FF9EB CRC64;


  Query Match             48.9%;  Score 42;  DB 2;  Length 406;
  Best Local Similarity   57.1%;  Pred. No. 87;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 IKFAAAHYNIEILK 18
           :|||   : ||||
Db      86 VKFANGEFKIEILK 99
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RESULT  8
Q9ERN4
ID   Q9ERN4      PRELIMINARY;      PRT:   558 AA.
AC   Q9ERN4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FUMARATE HYDRATASE CLASS I.
GN   FUMB.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN A3(2);
RA   Sweeper K.L., Harris D.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN A3(2);
RX   MEDLINE; 97000451; PubMed=8944436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.;
RA   Kinashi H., Bapwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL391754; CAC05880.1; -.
DR   InterPro; IPR000362; Fumarate_lyase.
DR   Pfam; PF00206; lyase_1; 1.
DR   PROSITE; PS00163; FUMARATE_LYASES; UNKNOWN_1.
SQ   SEQUENCE   558 AA;  60767 MW;  93BFD8A61DB062BE CRC64;


  Query Match             48.4%;  Score 42;  DB 2;  Length 558;
  Best Local Similarity   57.1%;  Pred. No. 53;
  Matches    8;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 EIKFAAAHYNIEI 16
           :| |:|:|||  ||
Db     244 KIAKYASAHYIDEI 257


RESULT  9
Q01480
ID   Q01480      PRELIMINARY;      PRT:  1858 AA.
AC   Q01480;
DT   01-NOV-1990 (TrEMBLrel. 01, Created)
DT   01-NOV-1990 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1990 (TrEMBLrel. 08, Last annotation update)
DE   APOLIPOPROTEIN B (FRAGMENT).
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER.
RX   MEDLINE; 95324549; PubMed=7541449;
RA   Babin P.J., Deryckere F., Gannon F.;
RT   "Presence of an extended duplication in the putative low density
RT   lipoprotein receptor binding domain of apolipoprotein B: Cloning and
RT   characterization of the domain in salmon.";
RL   Eur. J. Biochem. 230:45-51(1995).
DR   EMBL; X81856; CAA57449.1; -.
KW   Lipoprotein.
FT   NON_TER       1       1
SQ   SEQUENCE   1058 AA;  119924 MW;  5F46B2A5A1DB54CE CRC64;


  Query Match             48.4%;  Score 42;  DB 13;  Length 1058;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 IIKFAAAHYNIEIL 17
           |:|   ||| |:|:
Db     127 IVKAIIAHYIIDIV 140


RESULT  10
Q98IF0
ID   Q98IF0      PRELIMINARY;      PRT:  1187 AA.
AC   Q98IF0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CD11 2.
GN   CIA2.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL EXUDATE CELLS;
RA   Kimura M., Fujiki K., Nakao M.;
RT   "Molecular cloning of a leukocyte integrin from the common carp.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB048537; BAB39135.1; -.
SQ   SEQUENCE   1187 AA;  131778 MW;  85ED0C7AB0681C79 CRC64;


  Query Match             48.4%;  Score 42;  DB 13;  Length 1187;
  Best Local Similarity   61.5%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 IIKFAAAHYNIEI 16
           :|:|||  ::|||
Db     195 SIKFAAVQFSIEI 207


RESULT  11
Q19319
ID   Q19319      PRELIMINARY;      PRT:  4307 AA.
AC   Q19319; Q19785; Q21606;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   HYPOTHETICAL 479.0 KDA PROTEIN F25F2.2 IN CHROMOSOME III.
GN   F25F2.2.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN BRISTOL N2;
RA   Ainscough R.;
RL   Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
CC   !  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   !  SIMILARITY: TO THE CADHERIN FAMILY.
DR   EMBL; Z35662; CAA84721.1; -.
DR   EMBL; Z35599; CAA84721.1; JOINED.
DR   EMBL; Z34802; CAA84721.1; JOINED.
DR   EMBL; Z35599; CAA84661.1; -.
DR   EMBL; Z35662; CAA84661.1; JOINED.
DR   EMBL; Z34802; CAA84661.1; JOINED.
DR   EMBL; Z34802; CAA84439.1; -.
DR   EMBL; Z35599; CAA84439.1; JOINED.
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DR   EMBL; 245662; CAA84339.1; JOINED.
DR   HSSP; P15116; 1NCH.
DR   WormPep; F25F2.2; CE00961.
DR   InterPro; IPR002126; Cadherin.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001791; Laminin_G.
DR   Pfam; PF00028; cadherin; 24.
DR   Pfam; PF00008; EGF; 3.
DR   Pfam; PF00054; laminin_G; 1.
DR   PRINTS; PR00205; CADHERIN
DR   SMART; SM00112; CA; 28.
DR   SMART; SM00181; EGF; 4.
DR   SMART; SM00001; EGF_like; 1
DR   SMART; SM00282; LamG; 1.
DR   PROSITE; PS00232; CADHERIN_1; 1.
DR   PROSITE; PS50268; CADHERIN_2; 28.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_4.
DR   PROSITE; PS01186; EGF_2; 2.
KW   Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein;
KW   Hypothetical protein; Repeat; Transmembrane.
SQ   SEQUENCE   4307 AA;  478964 MW;  2853A6D08266AE51 CRC64;


  Query Match             48.8%;  Score 42;  DB 5;  Length 4307;
  Best Local Similarity   54.5%;  Pred. No. 4.9e+02;
  Matches    6;  Conservative    4;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       6 KFAAAHYNIEI 16
           |:|:|:| |::
Db    1377 KFSASHYQIDV 1387


RESULT  12
Q9ARH0
ID   Q9ARH0      PRELIMINARY;      PRT;    98 AA.
AC   Q9ARH0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CYSTEINE PROTEINASE INHIBITOR.
OS   Dianthus caryophyllus (Carnation) (Clove pink).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
OX   NCBI_TaxID=3570;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sugawara H., Satoh S.;
RT   "Molecular cloning of a carnation cDNA encoding a cysteine p; Cellular
RT   inhibitor.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY028994; AAK30004.1; -.
SQ   SEQUENCE   98 AA;  10793 MW;  BF60160FF159B81A CRC64;


  Query Match             47.1%;  Score 41;  DB 1;  Length 98;
  Best Local Similarity   50.0%;  Pred. No. 12;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 EEFIKFAAAHYNIE 15
           :|  |||  |||::
Db      21 DELAKFAVDHYNSK 34


RESULT  13
Q9YDU4
ID   Q9YDU4      PRELIMINARY;      PRT;   233 AA.
AC   Q9YDU4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   HYPOTHETICAL 26.0 KDA PROTEIN APE0824.
GN   APE0824.
OS   Aeropyrum pernix.
OC   Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC   Aeropyrum.
OX   NCBI_TaxID=56636;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN K1;
RX   MEDLINE=99310339; PubMed=10382966;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA   Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., Kosugi H.,
RA   Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA   Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA   Yamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K.,
RA   Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT   "Complete genome sequence of an aerobic hyper thermophilic
RT   crenarchaeon, Aeropyrum pernix K1.";
RL   DNA Res. 6:83-101(1999).
DR   EMBL; AP000060; BAA79803.1; -.
DR   InterPro; IPR000150; Zn_Mlpeptidse.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   233 AA;  25954 MW;  7B6980168CA04905 CRC64;


  Query Match             47.1%;  Score 41;  DB 1;  Length 233;
  Best Local Similarity   42.9%;  Pred. No. 30;
  Matches    9;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 EEFIKFAAAHYNIEILK 18
           :| |:|  |||    |:|
Db      94 EEVIKFIVAHEVAHIVK 110


RESULT  14
O35251
ID   O35251      PRELIMINARY;      PRT;   426 AA.
AC   O35251;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN   VEGF-D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN SPRAGUE DAWLEY;
RX   MEDLINE=97349118; PubMed=9205122;
RA   Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
DR   EMBL; AP014827; AAB66557.1; -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   Prodom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00244; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   426 AA;  47112 MW;  1261AFA4735960C00 CRC64;


  Query Match             47.1%;  Score 41;  DB 11;  Length 426;
  Best Local Similarity   61.5%;  Pred. No. 44;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       6 KFAAAHYNIEILK 18
           :|||  |:|: |
Db      93 KFAAIFYDIEILK 105
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RESULT 15
P97046
ID   P97046       PRELIMINARY;       PRT;   458 AA.
AC   P97046;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED GROWTH FACTOR).
GN   VEGF D OR FIGF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=97030254; PubMed=8876195;
RA   Orlandini M., Marconcini L., Ferruzzi R., Oliviero S.;
RT   "Identification of a c-fos-induced gene that is related to the
RT   platelet-derived growth factor/vascular endothelial growth factor
RT   family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RX   MEDLINE=97340118; PubMed=9205122;
RA   Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
DR   EMBL; X94572; CAA64892.1; -.
DR   EMBL; DB0628; BAA14002.1; -.
DR   HSSP; P15692; 1VPF.
DR   MGD; MGI:108087; Figf.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   458 AA;  49908 MW;  6636B17FBF07037C CRC64;


  Query Match             47.1%;  Score 41;  DB 11;  Length 458;
  Best Local Similarity   61.5%;  Pred. No. 48;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        6 KEAAAHYNTEILK 18
            :|||  :|:| ||
Db       94 KEAAIFYDIEILK 106


Search completed: February 22, 2002, 15:37:58
Job time: 116 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 22, 2002, 15:36:27 ; Search time 1.17 Seconds
(without alignments)
64.893 Million cell updates/sec

Title: US-09-534-376A-5
Perfect score: 87
Sequence: 1 XEEIIKFAAAHYNTEILK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	98.9	419	1	VEGC_HUMAN	P49767 homo sapien
2	73	83.9	419	1	VEGC_MOUSE	P97953 mus musculu
3	45.5	52.3	1063	1	DPOM_CLAPU	P22473 clavicepa p
4	42	48.3	548	1	PDBP_[illegible]	[illegible]
5	41	47.1	450	1	DNAA_SPICI	P33826 spiroplasma
6	41	47.1	843	1	PULA_THEMA	O33843 thermotoga
7	40	46.0	188	1	SCYD_GLOLA	Q00455 glomerella
8	39.5	45.4	882	1	YBAH_SCHPO	Q42908 schizosacch
9	39	44.8	329	1	1329_ASPNG	P87015 african swi
10	39	44.8	783	1	YCJK_ECOLI	P42592 escherichia
11	38.5	44.3	754	1	BGLB_CLOIM	P14002 clostridium
12	38.5	44.3	1095	1	YOH5_YEAST	Q08234 saccharomyce
13	38	43.7	155	1	Y060_BORBU	O51087 borrelia bu
14	38	43.7	343	1	YD57_METJA	Q58752 methanococc
15	38	43.7	447	1	DNAA_SYNY3	P49995 synechocyst
16	38	43.7	447	1	PROA_METAC	Q9HIA1 methanosarc
17	38	43.7	651	1	VU47_HSV6G	P30005 human herpe
18	38	43.7	651	1	VU47_HSV6U	Q69093 human herpe
19	38	43.7	800	1	PTI1_YEAST	P06784 saccharomyc
20	38	43.7	2413	1	PR09_YEAST	P43634 saccharomyc
21	37.5	43.1	154	1	DAU1_DAUCA	Q04298 daucus caro
22	37.5	43.1	1157	1	DPOM_PODAN	Q01529 podospora a
23	37	42.5	174	1	KAD_NEIGT	Q59694 neisseria c
24	37	42.5	174	1	KAD_NEIFL	Q59596 neisseria f
25	37	42.5	174	1	KAD_NEILA	Q59615 neisseria l
26	37	42.5	174	1	KAD_NEIPH	Q59628 neisseria p
27	37	42.5	174	1	KAD_NEIPO	Q59627 neisseria p
28	37	42.5	215	1	KAD_NEIGO	P49979 neisseria g
29	37	42.5	215	1	KAD_NEIMA	P49980 neisseria m
30	37	42.5	215	1	KAD_NEIMU	P49981 neisseria m
31	37	42.5	310	1	PURU_MYCTU	O50455 mycobacteri
32	37	42.5	359	1	YHCK_BACSU	P54595 bacillus su
33	37	42.5	422	1	[illegible]	[illegible]
34	37	42.5	444	1	GRA1_BRARE	O93436 brachydanio
35	37	42.5	449	1	GRA1_HUMAN	P24815 homo sapien
36	37	42.5	457	1	GRA1_BOVIN	P57695 bos taurus
37	37	42.5	457	1	GRA1_MOUSE	Q64018 mus musculu
38	37	42.5	457	1	GRA1_RAT	P07727 rattus norv
39	37	42.5	464	1	GRA3_RAT	P24524 rattus norv
40	37	42.5	465	1	GRA3_HUMAN	O75811 homo sapien
41	37	42.5	473	1	MAIK_YEAST	P53338 saccharomyce
42	37	42.5	651	1	Y942_METJA	Q58852 methanococc
43	37	42.5	681	1	GTOA_HAEIN	P44573 haemophilus
44	37	42.5	834	1	RSG3_HUMAN	Q14644 homo sapien
45	37	42.5	834	1	RSG3_MOUSE	Q60790 mus musculu

ALIGNMENTS

RESULT 1
VEGC_HUMAN
ID VEGC_HUMAN STANDARD; PRT; 419 AA.
AC P49767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF C) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-
DE L).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 104-120.
RX MEDLINE=96178224; PubMed=8617204;
RA [illegible] V., Pajusola K., Pajusola A., Thiel T., Tatibana T., Kroll E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RT "A novel vascular endothelial growth factor, VEGF C, is a ligand for
RT the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL EMBO J. 15:290-298(1996).
RN [2]
RP ERRATUM.
RX MEDLINE=96203094; PubMed=8617600;
RA [illegible] V., Pajusola K., Pajusola A., Thiel T., Tatibana T., Kroll E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RL EMBO J. 15:1751-1751(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96412526; PubMed=8700872;
RA Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RT "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Fowler P.S., Long A.L., Greco R.,
RA Burgess P., Giannotti J., Ciarletta A., Hennessey D., Kovacic S.,
RA Fitzgerald M., Scaltreto H., Welch N., Neben S., Finnerty H.,
RA Zeliner E., Ward J., Nienhuis E., Carraway R., Turner K.;
RA Wood C.R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH.
CC ! SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC ! PTM: PROBABLY PROTEOLYTICALLY PROCESSED IN THE C TERMINUS.
CC ! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC ---------- [illegible]

```
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X94216; CAA64007.1;  -.
DR   EMBL; U43142; AAA96214.1;  -.
DR   EMBL; U58111; AAB02609.1;  -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601528; -.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL        1      ?       POTENTIAL.
FT   PROPEP        ?    102       POTENTIAL.
FT   CHAIN       103    419       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN      275    365       4 X 24 AA TANDEM REPEATS.
FT   REPEAT      275    298       1.
FT   REPEAT      299    322       2.
FT   REPEAT      323    346       3.
FT   REPEAT      347    365       4 (PARTIAL).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   419 AA;  46884 MW;  9F5987F9DB03E14F CRC64;


  Query Match             98.0%;  Score 806;  DB 1;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 2e-07;
  Matches  147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           |||||||||||||||||
Db     104 EEIIKFAAAHYNIEILK 120


RESULT   2
VEGF_MOUSE
ID   VEGF_MOUSE     STANDARD;      PRT:   419 AA.
AC   P97953;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND)
DE   (FLT4-L).
GN   VEGFC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=97164067; PubMed=9012504;
RA   Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA   Joukov V., Alitalo K.;
RT   "VEGF-C receptor binding and pattern of expression with VEGFR-3
RT   suggests a role in lymphatic vascular development.";
RL   Development 122:3829-3837(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=97088332; PubMed=9217416;
RA   Fitz L.J., Morris J.F., Fowler P., Long A., Burgess F., Grosse F.,
RA   Ward L., Gasteiger E., Nickbarg E., Kovacevic S., Clark R.A.,
RA   Giannotti J., Finnerty H., Zollner R., Beier D.R., Lesk L.V.,
RA   Turner K.J., Wood C.R.;
RT   "Characterization of murine Flt4 ligand/VEGF-C.";
RL   Oncogene 15:613-618(1997).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR   EMBL; U43620; AAC52984.1;  -.
DR   EMBL; U58112; AAB46707.1;  -.
DR   HSSP; P15692; 1VPF.
DR   MGD; MGI:109124; Vegfc.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL        1      ?       POTENTIAL.
FT   PROPEP        ?     98       POTENTIAL.
FT   CHAIN        99    419       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN      271    361       4 X 24 AA TANDEM REPEATS.
FT   REPEAT      271    294       1.
FT   REPEAT      295    318       2.
FT   REPEAT      319    342       3.
FT   REPEAT      343    361       4 (PARTIAL).
FT   CARBOHYD    171    171       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    236    236       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   419 AA;  46471 MW;  D9D6DD3CE0C65D6D CRC64;


  Query Match             83.9%;  Score 74;  DB 1;  Length 419;
  Best Local Similarity   81.2%;  Pred. No. 4.5e-05;
  Matches   13;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 EIIKFAAAHYNIEILK 18
           :::|||||||||||||||
Db     101 DVVKFAAAHYNIEILK 116


RESULT   3
DPOM_CLAPU
ID   DPOM_CLAPU     STANDARD;      PRT:  1094 AA.
AC   P22375;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   PROBABLE DNA POLYMERASE (EC 2.7.7.7).
OS   Claviceps purpurea (Ergot fungus).
OG   Mitochondrion.
OG   Plasmid p4IKI.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreales; Clavicipitaceae; Claviceps.
OX   NCBI_TaxID=5111;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RX   MEDLINE=89063522; PubMed=2770691;
RA   Oeser B., Tudzynski P.;
RT   "The linear mitochondrial plasmid p4IKI of the phytopathogenic fungus
RT   Claviceps purpurea may code for a DNA polymerase and an RNA
RT   polymerase.";
RL   Mol. Gen. Genet. 217:132-140(1989).
CC   -!- CATALYTIC ACTIVITY: N-DEOXYNUCLEOSIDE TRIPHOSPHATE +
CC       N-DEOXYRIBONUCLEOTIDE = DNA(N).
```

```
CC    -!- MICROBIOLOGY: DNA POLYMERASE REQUIRED FOR DNA REPLICATION
CC        (BY SIMILARITY).
CC    -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE B FAMILY, SIG-NG, I.
CC        DNA POLYMERASE OF OTHER FUNGAL AND PLANTS MITOCHONDRIAL PLASMIDS.
CC    ---------- ---------- ---------- ---------- ---------- ----------
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CC    ---------- ---------- ---------- ---------- ---------- ----------
DR    EMBL; X15648; -; NOT_ANNOTATED_CDS.
DR    PIR; JQ0301; JQ0301.
DR    InterPro; IPR002064; DNA_pol_B.
DR    PRINTS; PR00106; DNAPOLB.
DR    SMART; SM00486; POLBc; 1.
DR    PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW    Transferase; DNA-directed DNA polymerase; DNA replication;
KW    DNA-binding; Plasmid; Mitochondrion.
SQ    SEQUENCE   1063 AA;  122540 MW;  4B50218F8F6E3179 CRC64;


  Query Match             52.3%;  Score 45.5;  DB 1;  Length 1,063;
  Best Local Similarity   58.8%;  Pred. No. 5.4;
  Matches   10;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       3 EFIKFAAAH-YNIEILK 18
           : ::|| || |  ||:|
Db     745 EELKFAVAHGYEVEIIK 761


RESULT   4
FUMB_ECOLI
ID   FUMB_ECOLI     STANDARD;      PRT;   548 AA.
AC   P14407; P78139;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   FUMARATE HYDRATASE CLASS I, ANAEROBIC (EC 4.2.1.2) (FUMARASE).
GN   FUMB OR B4122.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN K12;
RX   MEDLINE 90255127; PubMed 2099658;
RA   Boll P.T., Andrews S.C., Sivik M.N., Quail J.R.;
RT   "Nucleotide sequence of the FNR-regulated fumarase gene (fumB) of
RT   Escherichia coli K-12.";
RL   J. Bacteriol. 171:3494-3503(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN K12 / MG1655;
RX   MEDLINE 95334362; PubMed 7618843;
RA   Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA   Blattner F.R.;
RT   "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT   region from 92.8 through 100 minutes.";
RL   Nucleic Acids Res. 23:2105-2119(1995).
CC   -!- FUNCTION: IT FUNCTIONS IN THE CONVERSION OF FUMARATE TO L-MALATE AS AN
CC       ANAEROBIC ELECTRON ACCEPTOR.
CC   -!- CATALYTIC ACTIVITY: L-MALATE = FUMARATE + H(2)O.
CC   -!- COFACTOR: BINDS A 4FE-4S CLUSTER.
CC   -!- ENZYME REGULATION: SUBJECT TO ANAEROBIC REPRESSION.
CC   -!- PATHWAY: FERMENTATIVE PATHWAY THAT LEADS TO THE PRODUCTION OF
CC       SUCCINATE.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SIMILARITY: TO OTHER THERMOLABILE CLASS I FUMARASES.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; M27058; AAA24927.1; -.
DR   EMBL; U14003; AAA97022.1; -.
DR   PIR; B44511; B44511.
DR   EcoGene; EG10357; fumB.
DR   InterPro; IPR000362; Fumarate_lyase.
DR   Pfam; PF00206; lyase_1; 1.
DR   PROSITE; PS00163; FUMARATE_LYASES; 1.
KW   Lyase; Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S;
KW   Complete proteome.
FT   METAL       318    318       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   ACT_SITE    327    327       POTENTIAL.
FT   BINDING     463    463       CARBOXYL GROUP (POTENTIAL).
FT   CONFLICT     50     50       V -> L (IN REF. 2, AAC77083).
SQ   SEQUENCE   548 AA;  60091 MW;  336854D8FA5551AB CRC64;


  Query Match             48.8%;  Score 42;  DB 1;  Length 548;
  Best Local Similarity   50.0%;  Pred. No. 11;
  Matches    7;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 EFIKFAAAHYNIEI 16
           :|:| |:||| |:
Db     243 KIVKLASAHYYDEL 256


RESULT   5
DNAA_SPICI
ID   DNAA_SPICI     STANDARD;      PRT;   450 AA.
AC   P34028;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
GN   DNAA.
OS   Spiroplasma citri.
OC   Bacteria; Firmicutes, Bacillus/Clostridium group; Mollicutes;
OC   Spiroplasmataceae; Spiroplasma.
OX   NCBI_TaxID=2133;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN ATCC 27556 / R8A2;
RX   MEDLINE 94290261; PubMed 7764984;
RA   Ye F., Renaudin J., Bove J.M., Laigret F.;
RT   "Cloning and sequencing of the replication origin (oriC) of the
RT   Spiroplasma citri chromosome and construction of autonomously
RT   replicating artificial plasmids.";
RL   Curr. Microbiol. 29:25-29(1994).
RN   [2]
RP   SEQUENCE OF 147-411 FROM N.A.
RC   STRAIN ATCC 27556 / R8A2;
RX   MEDLINE 94109679; PubMed 8282191;
RA   Saeki K., Miyata M., Fukumura T.;
RT   "Comparison of the conserved region in the dnaA gene from three
RT   mollicute species.";
RL   FEMS Microbiol. Lett. 114:229-233(1993).
CC   -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
CC       OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION:
CC       IT BINDS SPECIFICALLY DOUBLE STRANDED DNA AT A 9 BP CONSENSUS
CC       (DNAA B.X., 5' TTATC[C/A,A]CA,A 3'. DNAA BINDS 1 ATP AND 10
CC       ACIDIC PHOSPHOLIPIDS.
CC   -!- SIMILARITY: BELONGS TO THE DNAA FAMILY.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC
DR   EMBL; Z19108; CAA79521.1;  -.
DR   EMBL; D14985; BAA03630.1;  -.
DR   PIR; S35732; S35732.
DR   InterPro; IPR001957; Rec DnaA.
DR   Pfam; PF00308; bac_dnaA; 1.
DR   PRINTS; PR00051; DNAA.
DR   PROSITE; PS01008; DNAA; 1.
KW   DNA replication; DNA binding; ATP binding.
FT   NP_BIND     146    153       ATP (POTENTIAL).
SQ   SEQUENCE   450 AA;  51547 MW;  C401E70015FE0961 CRC64;


  Query Match             47.1%;  Score 41;  DB 1;  Length 450;
  Best Local Similarity   85.3%;  Pred. No. 13;
  Matches    6;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEILK 18
           ||:::| | :|:|:|| |
Db     298 EESLEETAINENDVRK 314


RESULT  6
PULA_THEMA
ID   PULA_THEMA      STANDARD;      PRT;   843 AA.
AC   Q53840;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   PULLULANASE PRECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN END-  1,  ALPHA-
DE   -GLUCOSIDASE) (PULLULAN 6-GLUCANOHYDROLASE).
GN   PULA OR TM1845.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogales; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN MSB8 / DSM 3109;
RX   MEDLINE=98115241; PubMed=9451451;
RA   Bibel M., Brettl C., Gosslar U., Kriegshauser G., Liebl W.;
RT   "Isolation and analysis of genes for amylolytic enzymes of the
RT   hyperthermophilic bacterium Thermotoga maritima.";
RL   FEMS Microbiol. Lett. 158:9-15(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN MSB8 / DSM 3109;
RX   MEDLINE=99287436; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
CC    -!- CATALYTIC ACTIVITY: [illegible] ENZYME, WITH HYDRO
CC        (1-6) ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH.
CC        FORMATION OF...
CC    -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES. A.K.A.
CC        KNOWN AS THE ALPHA AMYLASE FAMILY.
CC
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CC
DR   EMBL; AJ002987; CAA04522.1;  -.
DR   EMBL; AF007021; AAD09607.1;  -.
DR   TIGR; TM1845;  -.
DR   InterPro; IPR000461; Alpha-amylase.
DR   Pfam; PF00128; alpha-amylase; 1.
KW   Hydrolase; Glycosidase; Signal; Complete proteome.
FT   SIGNAL      1     19       POTENTIAL.
FT   CHAIN      20    843       PULLULANASE.
FT   ACT_SITE   535    535       BY SIMILARITY.
FT   ACT_SITE   564    564       BY SIMILARITY.
FT   ACT_SITE   652    652       BY SIMILARITY.
SQ   SEQUENCE   843 AA;  96261 MW;  C42D0E2A6C54EE77 CRC64;


  Query Match             47.1%;  Score 41;  DB 1;  Length 843;
  Best Local Similarity   66.7%;  Pred. No. 2.5;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYN 13
           :|:|:||| | |
Db     642 EEIINYAACHDN 653


RESULT  7
SCYD_GLOLA
ID   SCYD_GLOLA      STANDARD;      PRT;   188 AA.
AC   Q00456;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   SCYTALONE DEHYDRATASE (EC 4.2.1.94).
GN   SCD1.
OS   Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
OS   lagenarium).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC   mitosporic Phyllachoraceae; Colletotrichum.
OX   NCBI_TaxID=5462;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1-1;
RX   MEDLINE=97111971; PubMed=8955707;
RA   Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.;
RT   "Cloning and structural analysis of the melanin biosynthesis SCD1
RT   gene encoding scytalone dehydratase in Colletotrichum lagenarium.";
RL   Appl. Environ. Microbiol. 62:4340-4344(1996).
CC    -!- FUNCTION: CATALYZES TWO STEPS IN MELANIN BIOSYNTHESIS, PER M
CC        SCYTALONE. THEY ARE TWO DEHYDRATION STEPS AND ONE REDUCTION STEP TO
CC        YIELD MELANIN.
CC    -!- CATALYTIC ACTIVITY: SCYTALONE = 1,3,8-TRIHYDROXYNAPHTHALENE +
CC        H(2)O.
CC    -!- PATHWAY: BIOSYNTHESIS OF FUNGAL MELANIN.
CC    -!- SUBUNIT: HOMODIMER. EACH SUBUNIT CONTAINS AN ACTIVE SITE, LOCATED
CC        IN THE CENTRAL PART OF THE HYDROPHOBIC CORE OF THE MONOMER, WHICH
CC        FUNCTIONS INDEPENDENTLY (BY SIMILARITY).
CC
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CC
DR   EMBL; D86079; BAA13009.1;  -.
DR   HSSP; P79211; 1STD.
KW   Lyase; Melanin biosynthesis.
SQ   SEQUENCE   188 AA;  21607 MW;  A58F3EB64043218EFA CRC64;


  Query Match             36.3%;  Score 40;  DB 1;  Length 188;
```

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  Best Local Similarity   80.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAH 11
           |:|||||||
Db     179 EKEIKFAAAH 188


RESULT  8
YBAH_SCHPO
ID   YBAH_SCHPO     STANDARD;      PRT:   882 AA.
AC   Q42938;
DT   1-JAN-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   HYPOTHETICAL 99.0 KDA PROTEIN C119.17 IN CHROMOSOME II.
GN   SPBC119.17.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN 972;
RA   Wood V., Rajandream M.A., Barrell B.G., Skelton J., Chandler C.M.;
RL   Submitted (MAR 1998) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; AL022117; CAA17332.3; -.
DR   InterPro; IPR001431; Peptidase_M16.
DR   Pfam; PF00675; Peptidase_M16; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   882 AA;  98970 MW;  6F1DA9A3467170C0 CRC64;


  Query Match             45.4%;  Score 99.5;  DB 1;  Length 882;
  Best Local Similarity   47.4%;  Pred. No. 46;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    3;  Gaps    1;

Qy       2 EEIIKFAAAHY--NIEIL 17
           :| :|| :|:  : :||
Db     235 EELVKFHRSHYHPSNAKIL 254


RESULT  9
I329_ASFB7
ID   I329_ASFB7     STANDARD;      PRT:   329 AA.
AC   P27945;
DT   1-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   LATE PROTEIN I329L PRECURSOR.
GN   I329L.
OS   African swine fever virus (strain BA71V) (ASFV).
OC   Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
OC   African swine fever-like viruses.
OX   NCBI_TaxID=10498;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92087485; PubMed=1309292;
RA   Rodriguez J.M., Salas M.L., Vinuela E.;
RT   "Genes homologous to ubiquitin-conjugating proteins and eukaryotic
RT   transcription factor SII in African swine fever virus.";
RL   Virology 186:340-52(1992).
RN   [2]
RP   COMPLETE GENOME.
RA   Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
RA   Rodriguez J.F., Vinuela E.;
RT   "Analysis of the complete nucleotide sequence of African swine fever
RT   virus.";
RL   Virology 208:249-278(1995).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE.
CC   -!- DEVELOPMENTAL STAGE: LATE IN INFECTION.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; M77121; AAA42702.1; -.
DR   EMBL; U18466; AAA65569.1; -.
DR   PIR; I39118; WMXFB4.
KW   Late protein; Signal; Transmembrane; Glycoprotein.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    329       LATE PROTEIN I329L.
FT   DOMAIN      18    239       EXTRACELLULAR.
FT   TRANSMEM   240    260       POTENTIAL.
FT   DOMAIN     261    329       CYTOPLASMIC.
FT   CARBOHYD    52     52       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    59     59       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    44     44       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    76     76       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    82     82       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   101    101       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   165    165       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   254    254       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   329 AA;  38542 MW;  B480F6CACA4273FB CRC64;


  Query Match             44.8%;  Score 98;  DB 1;  Length 329;
  Best Local Similarity   87.5%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      11 HYNIEILK 18
           :|:| |||
Db      80 HYNISILK 87


RESULT  10
YGJK_ECOLI
ID   YGJK_ECOLI     STANDARD;      PRT:   783 AA.
AC   P42592;
DT   01-NOV 1995 (Rel. 32, Created)
DT   01-NOV 1995 (Rel. 32, Last sequence update)
DT   20-AUG 2001 (Rel. 40, Last annotation update)
DE   HYPOTHETICAL PROTEIN YGJK PRECURSOR.
GN   YGJK OR B3080.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN K12 / MG1655;
RX   MEDLINE 97120417; PubMed 9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   -----------------------------------------------------------------------
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```

DR EMBL; D13900; BAA03081.1; -.
DR EMBL; AE000396; AAC76115.1; -.
DR EcoGene; EG12722; yqjK.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 783 HYPOTHETICAL PROTEIN YQJK.
SQ SEQUENCE 760 AA; 88621 MW; AE4C47BFB78EC82B CRC64;

Query Match 44.8%; Score 89; DB 1; Length 760;
Best Local Similarity 58.4%; Pred. No. 5.2;
Matches 73; Conservative 23; Mismatches 9; Indels 0; Gaps 0;

Qy 7 FAAAHYNIEILK 18
|| |||| ||:|
Db 453 FAMAHENPDIAK 464

RESULT 11
YGLB_CLOTM
ID YGLB_CLOTM STANDARD; PRT; 754 AA.
AC P14002;
DT 01-JAN-1990 (Rel. 14, Created)
DT 01-JAN-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE THERMOSTABLE BETA-GLYCOSIDASE B (EC 3.2.1.21) (GENTIOBIASE)
DE (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE).
GN BGLB.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 27405 / NCIB 9035;
RX MEDLINE=80364694; PubMed=7505054;
RA Graebnitz F., Buecknagel K.P., Seiss M., Staudenbauer W.L.;
RT "Nucleotide sequence of the Clostridium thermocellum beta-glucosidase
RT encoding thermostable beta-glucosidase B: homology to other
RT beta-glucosidases.";
RL Mol. Gen. Genet. 217:70-76(1989).
CC ! CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.
CC ! PATHWAY: CELLULOSE DEGRADATION.
CC ! SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
CC
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CC
DR EMBL; X15644; CAA33665.1; -.
DR PIR; S04381; S04381.
DR InterPro; IPR001764; Glyco_hydro_3.
DR InterPro; IPR002772; Glyco_hydro_3C.
DR Pfam; PF00933; Glyco_hydro_3; 1.
DR Pfam; PF01915; Glyco_hydro_3_C; 1.
DR PRINTS; PR00133; GLHYDROLASE3.
DR PROSITE; PS00775; GLYCOSYL_HYDRO_F3; 1.
KW Hydrolase; Glycosidase; Cellulose degradation.
FT ACT_SITE 281 281 BY SIMILARITY.
SQ SEQUENCE 754 AA; 84166 MW; A9CE0498B7C0A9A0 CRC64;

Query Match 44.4%; Score 88.5; DB 1; Length 754;
Best Local Similarity 45.0%; Pred. No. 6.1;
Matches 9; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

Qy 2 FEILKF AAAHYNIEI 16
|:|:| | |:||:|
Db 615 LKIVIFILGKRAFAYYN?QI 638

RESULT 12
YOR5_YEAST
ID YOR5_YEAST STANDARD; PRT; 1095 AA.
AC Q08234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE ATP-DEPENDENT TRANSPORTER YOR075W.
GN YOR075W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97521007; PubMed=9278509;
RA Iserentant D., Fink G.R.;
RT "Secretion-dependent alterations of Ty1 protein processing.";
RL Mol. Cell. Biol. 17:5876-5887(1997).
CC ! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC ! SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). MDR SUBFAMILY.
CC
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CC
DR EMBL; Z74017; CAA99085.1; ALT_INIT.
DR SGD; S0005435; YOR075W.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001687; ATP/GTP-A.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS50211; ABC_TRANSPORTER; 1.
KW Hypothetical protein; ATP-binding; Transmembrane; Glycoprotein;
KW Transport.
FT TRANSMEM 6 26 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 264 284 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 454 474 POTENTIAL.
FT TRANSMEM 406 426 POTENTIAL.
FT TRANSMEM 840 860 POTENTIAL.
FT TRANSMEM 871 891 POTENTIAL.
FT TRANSMEM 922 942 POTENTIAL.
FT TRANSMEM 949 969 POTENTIAL.
FT TRANSMEM 978 998 POTENTIAL.
FT TRANSMEM 1009 1029 POTENTIAL.
FT TRANSMEM 1068 1088 POTENTIAL.
FT NP_BIND 528 545 ATP (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 784 784 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 863 863 N-LINKED (GLCNAC...) (POTENTIAL).

```
SQ   SEQUENCE   1095 AA;  123507 MW;  D6D5C114A5EEA982 CRC64;


  Query Match             44.4%;  Score 88.5;  DB 1;  Length 1 95;
  Best Local Similarity   52.9%;  Pred. No. 91;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       2 EEIIKFAAAA  HYNIE 15
           ||:|:|||:   |: ||
Db     592 KEILKYAAALKLRHLIE 608


RESULT  13
Y360_BORBU
ID   Y360_BORBU     STANDARD;      PRT;   155 AA.
AC   O51382;
DT   30-MAY 2000 (Rel. 39, Created)
DT   30-MAY 2000 (Rel. 39, Last sequence update)
DT   20-AUG 2001 (Rel. 40, Last annotation update)
DE   HYPOTHETICAL PROTEIN BB0060.
GN   BB0060.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35210 / B31;
RX   MEDLINE=98055443; PubMed=9438685;
RA   Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA   Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA   Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA   Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA   van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA   Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA   Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA   Smith H.O., Venter J.C.;
RT   "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT   burgdorferi.";
RL   Nature 390:580-586(1997).
CC   -!- SIMILARITY: BELONGS TO THE UPF0054 FAMILY.
CC   ----------- -- -- ------ ---- -- ------- -- - - - - - - - - - - - -
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CC   ----------- -- -- ------ ---- -- ------- -- - - - - - - - - - - - -
DR   EMBL; AE001169; AAC66448.1; -.
DR   TIGR; BB0060; -.
DR   InterPro; IPR002906; UPF0054.
DR   Pfam; PF02130; UPF0054; 1.
DR   ProDom; PD005688; UPF0054; 1.
DR   PROSITE; PS01309; UPF0054; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   155 AA;  18259 MW;  CB7E687B02BE4ABE CRC64;


  Query Match             43.7%;  Score 88;  DB 1;  Length 155;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    2;  Gaps    0;

Qy       3 EEIKFAAAHYNIEI 16
           |:|||:  :|:||
Db      97 EYLKFSAQEFNVEI 110


RESULT  14
YE57_MELJA
ID   YE57_MELJA     STANDARD;      PRT;   443 AA.
AC   Q58852;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   PUTATIVE POTASSIUM CHANNEL PROTEIN MJ1457.
GN   MJ1457.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LAL 1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0038.1.
CC   -!- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
CC   ----------- -- -- ------ ---- -- ------- -- - - - - - - - - - - - -
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CC   ----------- -- -- ------ ---- -- ------- -- - - - - - - - - - - - -
DR   EMBL; D67575; AAB99365.1; -.
DR   TIGR; MJ1457; -.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003148; KIN.
DR   InterPro; IPR000595; TrkA_Kuptake.
DR   Pfam; PF02254; KIN; 1.
DR   Pfam; PF02080; TrkA; 1.
KW   Hypothetical protein; Transmembrane; Transport; Ion transport;
KW   Ionic channel; Complete proteome.
FT   TRANSMEM      8     28       POTENTIAL.
FT   TRANSMEM     30     50       POTENTIAL.
FT   TRANSMEM     62     82       POTENTIAL.
SQ   SEQUENCE   443 AA;  48883 MW;  6123B0C001B54C4 CRC64;


  Query Match             43.7%;  Score 88;  DB 1;  Length 443;
  Best Local Similarity   47.1%;  Pred. No. 32;
  Matches    8;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           || | | |   | :||
Db     128 EENIETIAIDINIEDVK 144


RESULT  15
DNAA_SYNY3
ID   DNAA_SYNY3     STANDARD;      PRT;   447 AA.
AC   P49005; P73750;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
GN   DNAA OR SLL0848.
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE; 96362716; PubMed=8645812;
RA   Richter S., Messer W.;
RT   "Genetic structure of the dnaA region of the cyanobacterium
RT   Synechocystis sp. strain PCC6803.";
RL   J. Bacteriol. 177:4249-4251(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
CC    !  FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
CC       OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION;
CC       IT BINDS SPECIFICALLY DOUBLE STRANDED DNA AT A 9 BP CONSENSUS
CC       (DNAA BOX): 5' TTATC(C/A)A(C/A)A 3'. DNAA BINDS TO ATP AND TO
CC       ACIDIC PHOSPHOLIPIDS (BY SIMILARITY).
CC    !  SIMILARITY: BELONGS TO THE DNAA FAMILY.
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CC
DR   EMBL; L39058; AAA85913.1; -.
DR   EMBL; D90906; BAA17801.1; -.
DR   InterPro; IPR001957; Bac_DnaA.
DR   Pfam; PF00308; bac_dnaA; 1.
DR   PRINTS; PR00051; DNAA.
DR   PROSITE; PS01008; DNAA; 1.
KW   DNA replication; DNA binding; ATP binding; Complete proteome.
FT   NP_BIND      147     154       ATP (POTENTIAL).
FT   CONFLICT     118     125       VGPTNRMA -> WAHQSHC (IN REF. 1).
FT   CONFLICT     297     297       I -> M (IN REF. 1).
SQ   SEQUENCE   447 AA;  50050 MW;  8AC7A6BD6C70BD3BF CRC64;


  Query Match             43.7%;  Score 88;  DB 1;  Length 447;
  Best Local Similarity   40.0%;  Pred. No. 4.2;
  Matches    96;  Conservative    59;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 EETIKEAAAHYNIEI 16
           :| |:: |:|| : |
Db     294 KEVIEYIASHYISNI 308



Search completed: February 22, 2002, 15:38:14
Job time: 107 sec
```

GenCore version 4.5

Smith-Waterman protein search, using sw model

Run on: February 22, 2002, 15:35:12 ; Search time 1.221 Seconds
(without alignments)
2072.887 Million cell updates/sec

Title: US-09-534-376A-5
Perfect score: 87
Sequence: 1 XEEIIKFAAAHHYNIEILK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76173592 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	98.9	419	2	S69207	vascular endothelial
2	45.5	52.3	1097	2	JQ0381	hypothetical 127K
3	42	48.3	406	2	G70167	phosphoribosyl pyr
4	42	48.3	548	1	B44511	fumarate hydratase
5	42	48.3	548	2	E86167	hypothetical prote
6	42	48.3	1058	2	S65460	apolip protein B
7	42	48.3	4307	2	I20721	hypothetical prote
8	41	47.1	233	2	A72679	hypothetical prote
9	41	47.1	450	2	S35742	dnaA protein Spi
10	41	47.1	836	2	I32208	hypothetical pr to
11	41	47.1	843	2	H72264	putrescinase Ther
12	40	46.0	368	2	S72703	quinolinate synthe
13	40	46.0	765	2	G64502	hypothetical prote
14	39.5	45.4	992	2	I39435	hypothetical prote
15	39	44.8	234	2	G96721	probable glutathio
16	39	44.8	317	2	H72422	thioredoxin reduct
17	39	44.8	329	1	WMXFB4	15kDa protein - At
18	39	44.8	473	2	B85482	hypothetical prote
19	39	44.8	485	2	H72424	hypothetical prote
20	39	44.8	783	2	E65096	hypothetical 88.8K
21	39	44.8	783	2	A85969	probable isomerase
22	39	44.8	965	2	I39728	26S proteasome non
23	38.5	44.3	754	2	S04381	beta-glucosidase (
24	38.5	44.3	1294	2	S77699	probable nonmotor
25	38	43.7	33	2	PS0433	dystrophin - rabbi
26	38	43.7	155	2	D70107	Sulfolobus hypothet
27	38	43.7	273	1	S69189	nor related protei
28	38	43.7	329	2	I47419	hypothetical prote
29	38	43.7	332	2	D69200	dihydrodipicolinic
30	38	43.7	339	2	I39156	probable integral
31	38	43.7	343	2	D64469	potassium channel
32	38	43.7	447	2	S74846	replication initia
33	38	43.7	453	2	C40511	hypothetical prote
34	38	43.7	470	2	I41465	cell cycle protein
35	38	43.7	651	2	C56656	membrane glycoprot
36	38	43.7	800	2	S53079	HEXIS protein - y
37	38	43.7	803	2	I24685	hypothetical prote
38	38	43.7	861	2	I39781	probable large ATP
39	38	43.7	1091	2	I15564	hypothetical prot
40	38	43.7	2413	2	S54670	splicing factor PR
41	37.5	43.1	154	2	I14325	major allergen Lau
42	37.5	43.1	154	2	I14356	major allergen Lau
43	37.5	43.1	154	2	I14322	major root protein
44	37.5	43.1	168	2	I14302	pathogenesis relat
45	37.5	43.1	754	2	B69745	hypothetical prote

ALIGNMENTS

RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand; DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A;Reference number: S69207; MUID:96205064
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1774888; PIDN:CAA64007.1; PID:g221694; GI:g158
A;Note: the nucleotide sequence was submitted to the EMBL data library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the FLT4
A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown, not compared with conceptual translation.
A;Molecule type: mRNA
A;Residues: 70-419 <JOU1>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ... cDNA and
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: B01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U59111; NID:g1374426; PIDN:AAB02909.1; PID:g1374427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-reference: GDB:099088; OMIM:601528
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-102/Domain: propeptide #status predicted <PRO>

```
F;103-419/Product: vascular endothelial growth factor C #status experimental ; MAT

  Query Match             98.9%;  Score 86;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKFAAAHYNIEILK 18
           |||||||||||||||||
Db     104 EELIKFAAAHYNIEILK 120


RESULT   2
Y00301
hypothetical 1.7K protein   - yeast (Pichia) mitochondrion
C;Species: mitochondrion Claviceps purpurea (ergot fungus)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1999
C;Accession: Y00301
R;Esser, K.; Lojkowska, E.
Mol. Gen. Genet. 217, 132-140, 1989
A;Title: The linear mitochondrial plasmid pCLK1 of the phytopathogenic fungus Claviceps
A;Reference number: Y00301; MUID:89364677
A;Contents: Plasmid pCLK1, strain K
A;Accession: Y00301
A;Molecule type: DNA
A;Residues: 1-1997 <ESS
C;Comment: This protein is possibly DNA polymerase.
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: 4STA
C;Superfamily: Neurospora crassa mitochondrion plasmid pCLK1 DNA-directed DNA polymer
C;Keywords: mitochondrion


  Query Match             52.3%;  Score 45.5;  DB 2;  Length 1997;
  Best Local Similarity   58.8%;  Pred. No. 11;
  Matches   10;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       8 EELIKFAAAH YNIEILK 38
           | :|||: :| |  |:|
Db     779 EELKLAVAHCYEVEILK 795


RESULT   3
G70167
phosphoribosyl pyrophosphate synthetase (prs) homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: G70167
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, O.; Peterson, S.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
A;Reference number: A70100; MUID:98065943
A;Accession: G70167
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-406 <KIE>
A;Cross-references: GB:AE001156; GB:AE000784; NID:g2088415; PIDN:AAC66412.1; PID:g2088
A;Experimental source: strain B31


  Query Match             18.6%;  Score 16;  DB 2;  Length 406;
  Best Local Similarity   57.1%;  Pred. No. 16;
  Matches    8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 IKFAAAHYNIEILK 18
           :|||   : ||||
Db      86 VKFANGLEKIEILK 99


RESULT   4
B44511
fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
N;Alternate names: fumarase B
C;Species: Escherichia coli
C;Date: 03-Mar-1993 #sequence_revision 16-Oct-1997 #text_change 08-Jun-1999
C;Accession: A65222; B44511; S56351
R;Blattner, F.R.; Plunkett, G. III; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A65222
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-548 <BLA>
A;Cross-references: GB:AE000486; GB:U00006; NID:g1790563; PIDN:AAC77085.1; PID:g1790
A;Experimental source: strain K-12, substrain MG1655
R;Bell, P.J.; Andrews, S.C.; Sivak, M.N.; Guest, J.R.
J. Bacteriol. 171, 3494-3503, 1989
A;Title: Nucleotide sequence of the FNR-regulated fumarase gene (fumB) of Escherichia
A;Reference number: A44511; MUID:89255124
A;Accession: B44511
A;Molecule type: DNA
A;Residues: 1-49,'V',51-548 <BEL>
A;Cross-references: EMBL:M27858; NID:g146048; PIDN:AAA23827.1; PID:g146048
R;Burland, V.; Plunkett, G. III; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
A;Reference number: S56344; MUID:95334362
A;Accession: S56351
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-49,'X',51-548 <BUR>
A;Cross-references: EMBL:U14003; NID:g1262172; PIDN:AAA97027.1; PID:g536007
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Comments: In E. coli, three fumarate hydratase genes (fumA, fumB, and fumC) have been
 class I hydratase.
C;Genetics:
A;Gene: fumB
A;Map position: 93.5 min
C;Complex: homodimer
C;Function:
A;Description: catalyzes the stereospecific interconversion of fumarate and L-malate
A;Note: expressed at higher level under anaerobic conditions
C;Superfamily: iron-dependent fumarate hydratases; iron-dependent tartrate dehydratase
C;Keywords: 4Fe-4S; carbon-oxygen lyase; homodimer; hydro-lyase; iron-sulfur protein;
F;2-548/Product: fumarate hydratase fumB, iron-dependent #status predicted <MAT>
F;93-500/Domain: iron-dependent tartrate dehydratase alpha chain homology <IIHA
F;274-527/Domain: iron-dependent tartrate dehydratase beta chain homology <IIHB>


  Query Match             48.8%;  Score 42;  DB 1;  Length 548;
  Best Local Similarity   50.0%;  Pred. No. 22;
  Matches    7;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       8 EILIKFAAAHYNIEI 16
           :|:| |:|||  |:
Db     434 KIVKLASAHYYDEL 450


RESULT   5
E86107
hypothetical protein fumB [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 19-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E86107
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
illier, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodа
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: AH5480; MUID:21074995; PMID:11206551
A;Accession: E86107
```

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-548 <SI>
A;Cross-references: GB:AE000174; NID:g2190647; PIDN:AAC06211.1; GSPDB:GN00...; PWB:P7...
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: TumB
C;Superfamily: iron dependent fumarate hydratase; iron dependent fumarate dehydratase a...

Query Match 48.8%; Score 42; DB 2; Length 548;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 0;

Qy 3 EIIKFAAAHYNIEI 16
:|:| |:|:| :
Db 243 KIVKLASAHYYDEL 256

RESULT 6
S65460
apolipoprotein B - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 04-Dec 1997 #sequence_revision 12 Dec 1997 #text_change 15 Aug 1999
C;Accession: S65460; I51462
R;Babin, P.J.; Deryckere, F.; Gannon, F.
Eur. J. Biochem. 240, 45-51, 1995
A;Title: Presence of an extended duplication in the putative low density lipoprotein re...
A;Reference number: I51462; MUID:95324549
A;Accession: S65460
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1058 <BAB>
A;Cross-references: EMBL:X81058; NID:g585619; PIDN:CAA57114.1; GSPDB:...
A;Experimental source: liver
C;Genetics:
A;Gene: apoB
C;Superfamily: apolipoprotein B
C;Keywords: calcium; cholesterol metabolism; chylomicron; glycoprotein; intestine; LDL;

Query Match 48.8%; Score 42; DB 2; Length 1...
Best Local Similarity 50.0%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 0;

Qy 3 EIIKFAAAHYNIEILK 18
:|: |:|:| :|::
Db 127 IVKAIIAHYIIDIV 140

RESULT 7
I20721
hypothetical protein F25F2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct 1999 #sequence_revision 15 Oct 1999 #text_change 19 May 2000
C;Accession: I20721; I21443; I23842
R;Ainscough, R.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19414
A;Accession: I20721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4307 <WIL>
A;Cross-references: EMBL:Z35662; PIDN:CAA84721.1; GSPDB:GN...; ...
A;Experimental source: clone F10G11
R;Ainscough, R.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19419
A;Accession: I21443
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4307 <WIL>
A;Cross-references: EMBL:Z35660; PIDN:CAA84719.1; GSPDB:GN...; ...
A;Experimental source: clone F25F2
R;Sulston, J.
submitted to the EMBL Data Library, June 1994
A;Reference number: Z19806
A;Accession: I23842
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4307 <WIL>
A;Cross-references: EMBL:Z34802; PIDN:CAA84339.1; GSPDB:GN...; ...
A;Experimental source: clone M88
C;Genetics:
A;Gene: CESP:F25F2.2
A;Map position: 3
C;Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G r...
F;3761-3909/Domain: laminin G repeat homology <LGR>

Query Match 48.8%; Score 42; DB 2; Length 4307;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KFAAAHYNIEI 16
|||:||| |::
Db 1377 KFSASHYQIDV 1387

RESULT 8
G72675
hypothetical protein APE0824 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: G72675
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Ito-Yam...
Jin, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aero...
A;Reference number: A7450; MUID:99410339
A;Accession: G72675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <KAW>
A;Cross-references: GB:AP000060; NID:g5104188; PIDN:BAA79019.1; PID:g5104189; GP:...
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0824
C;Superfamily: Aeropyrum pernix hypothetical protein APE0824

Query Match 47.1%; Score 41; DB 2; Length 233;
Best Local Similarity 52.9%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 EEIIKFAAAHYNIEILK 18
|| ||| || |:|
Db 94 EEVIKFIVAHEVAHIVK 110

RESULT 9
S35732
dnaA protein - Spiroplasma citri
C;Species: Spiroplasma citri
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Feb-2...
C;Accession: S35732
R;Ye, F.; Labarre, F.; Bove, J.
submitted to the EMBL Data Library, December 1992
A;Description: Nucleotide sequence and genetic organization at the replication origin
A;Reference number: S35732
A;Accession: S35732
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <YEF>
A;Cross-references: EMBL:Z19108; NID:g49445; PIDN:CAA79521.1; PID:g49446

```
C;Genetics:
A;Genetic code: gpCA
C;Superfamily: replication initiation protein dnaA
C;Keywords: DNA binding; nucleotide binding; P loop
F,146-153/Region: nucleotide binding motif A (P loop)
F,208-212/Region: nucleotide binding motif B


  Query Match             47.1%;  Score 41;  DB 2;  Length [---];
  Best Local Similarity   35.0%;  Pred. No. 26;
  Matches    6;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEIIK 18
           ||:::|:|:::|:::| |
Db     298 EESGEFIALNENSDVPK 314


RESULT  10
I42298
hypothetical protein M151.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change [--]-[--]-1999
C;Accession: I42298
R;Sulston, J.; Waelia, D.
Submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid M151.
A;Reference number: Z21148
A;Accession: I42298
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-846 <SAI>
A;Cross-references: EMBL:AF024810; PIDN:AAB54778.1; GSPDB:GN[--]; [--]:M151.3
A;Experimental source: strain Bristol N2; clone M151
C;Genetics:
A;Gene: CESB:M151.3
A;Map position: X
A;Introns: 40/1  [--]-[--]  [--]/1  [--]-[--]  [--]/1  [--]-[--]  [--]/1  [--]-[--]  [--]/1


  Query Match             47.1%;  Score 41;  DB 2;  Length [--];
  Best Local Similarity   46.7%;  Pred. No. 51;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEI 16
           ||:|||  |::|:|:
Db     342 EEKLKEAEQHFRGEL 356


RESULT  11
H72504
probidanase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72504
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316
A;Accession: H72504
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1864 <AKN>
A;Cross-references: GB:AE001821; GB:AF000512; NID:g4980121; PIDN:AAD[--].1; PID:g[--]
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1845


  Query Match             47.1%;  Score 41;  DB 2;  Length 814;
  Best Local Similarity   66.7%;  Pred. No. 52;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEIIK 18
           ||:|:|:|:|:|:|:|
Db     [--] EEIINYAACHDNGFA 654


RESULT  12
S72703
quinolinate synthetase nadA - Mycobacterium leprae
N;Alternate names: lepB1170 C2_201 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Jul-1999
C;Accession: S72703
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1170.
A;Reference number: S72703
A;Accession: S72703
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <SMI>
A;Cross-references: EMBL:U00020; NID:g1067780; PIDN:AAA17067.1; PID:g467791
C;Genetics:
A;Gene: nadA
C;Superfamily: quinolinate synthetase A


  Query Match             46.0%;  Score 40;  DB 2;  Length 308;
  Best Local Similarity   47.1%;  Pred. No. 42;
  Matches    8;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEIIK 18
           |||:|:  |:  |:| |
Db     [--] EEIIVPGSVHEMAEIAK 116


RESULT  13
G64502
hypothetical protein MJ1626 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 15-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C;Accession: G64502
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Klenk, H.P.; Weidman, J.F.; Merrick, J.M.; Clayton, R.
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Berenbovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A;Reference number: A64300; MUID:96337999
A;Accession: G64502
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-765 <BUL>
A;Cross-references: GB:U67602; GB:L77117; NID:g1592214; PIDN:AAB99649.1; PID:g1500624
C;Genetics:
A;Map position: REV1602302 1600085


  Query Match             46.0%;  Score 40;  DB 2;  Length 765;
  Best Local Similarity   43.8%;  Pred. No. 74;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 EEIIKEAAAHYNIEIIL 17
           |:|:|:  :|:|:|::
Db     212 EESIKEIIKNYNSEMI 227


RESULT  14
T50415
hypothetical protein SPBC119.17 - fission yeast (Schizosaccharomyces pombe) (fragment
C;Species: Schizosaccharomyces pombe
C;Date: 03-Jan-1999 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T50415; T40545
```

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Bowman, S.
Submitted to the EMBL Data Library, March 1998
A;Reference number: Z21843
A;Accession: T39315
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-882 ;We ;
A;Cross-references: EMBL:AL022117; PID:CAA17052.1; GSPDB:GN=;; SPDB:SPBC119.11
A;Experimental source: strain 972h ; cosmid c119
R;Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Hunt, I.; Avos, S.J.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21646
A;Accession: T40545
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 883 992 ;LYN;
A;Cross-references: EMBL:AL110506; PID:CAB54806.1; GSPDB:GN=;; SPDB:SPAC577.01
A;Experimental source: strain 972h; cosmid c577
C;Genetics:
A;Gene: SPDB:SPBC119.17; SPDB:SPAC577.01
A;Map position: 2
A;Introns: 40/3

Query Match 45.4%; Score 39.5; DB 2; Length ??;
Best Local Similarity 47.4%; Prod. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EEIIKFAAABY NIEIL 17
|| :|| :|| | :||
Db 235 EELVKFHKSHYHPSNAKIL 253

RESULT 15
Q96721
probable glutathione transferase U17F4.4 [imported] Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Mar-2001
C;Accession: Q96721
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chunst, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.B.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Martin, F.; Marshall,
Rizzo, M.; Rooney, I.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: Q96721
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 ;SIG;
A;Cross-references: GB:AE005174; NID:g6588801; PIDN:AAF02981.1; GSPDB:GN=141
C;Genetics:
A;Gene: U17F4.4
A;Map position: 1
C;Superfamily: auxin induced protein

Query Match 44.8%; Score 39; DB 2; Length 234;
Best Local Similarity 41.2%; Prod. No. 29;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EEIIKFAAABYNIEIIK 18
|: :|| :|| | |
Db 218 EKLVQFARLKFNISIFK 234

Search completed: February 22, 2002, 15:47:28
Job time: 136 sec

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Run on: protein search, using sw model

Run time: February 22, 2002, 15:44:57 ; Search time 1.1 Seconds
(without alignments)
42.5+ Million cell updates/sec

Title: US-09-534-376A-5
Perfect score: 87
Sequence: 1 XEEIIKFAAAHYNIEIIK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503202 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB/pep_*
2: /cgn2_6/ptodata/1/ina/5B_COMB/pep_*
3: /cgn2_6/ptodata/1/ina/5C_COMB/pep_*
4: /cgn2_6/ptodata/1/ina/6A_COMB/pep_*
5: /cgn2_6/ptodata/1/ina/6B_COMB/pep_*
6: /cgn2_6/ptodata/backfiles1/pep/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	98.9	17	4	US-08-795-430-9	Sequence 9, Appli
2	86	98.9	18	4	US-08-795-430-5	Sequence 5, Appli
3	86	98.9	18	4	US-08-510-133A-18	Sequence 18, Appl
4	86	98.9	18	4	US-08-585-895-18	Sequence 18, Appl
5	86	98.9	854	2	US-08-999-811-3	Sequence 3, Appli
6	86	98.9	350	2	US-08-824-996-2	Sequence 2, Appli
7	86	98.9	350	3	US-09-042-105-4	Sequence 4, Appli
8	86	98.9	350	4	US-08-510-133A-33	Sequence 33, Appl
9	86	98.9	350	4	US-08-585-895-33	Sequence 33, Appl
10	86	98.9	419	2	US-08-999-811-2	Sequence 2, Appli
11	86	98.9	419	3	US-09-042-105-2	Sequence 2, Appli
12	86	98.9	419	3	US-09-042-105-18	Sequence 18, Appl
13	86	98.9	419	4	US-08-795-430-8	Sequence 8, Appli
14	86	98.9	419	4	US-08-510-133A-35	Sequence 35, Appl
15	86	98.9	419	5	PCT-US96-00001-2	Sequence 2, Appli
16	73	83.9	415	4	US-08-795-430-11	Sequence 11, Appl
17	69	79.3	419	4	US-08-795-430-12	Sequence 12, Appl
18	44	50.6	8	4	US-08-510-133A-23	Sequence 23, Appl
19	44	50.6	8	4	US-08-585-895-23	Sequence 23, Appl
20	41	47.1	321	4	US-08-915-795-9	Sequence 9, Appli
21	41	47.1	858	4	US-08-915-795-8	Sequence 8, Appli
22	41	47.1	862	1	US-08-415-221-20	Sequence 20, Appl
23	39	44.8	7	4	US-08-510-133A-20	Sequence 20, Appl
24	39	44.8	7	4	US-08-585-895-20	Sequence 20, Appl
25	37.5	43.1	154	1	US-08-363-010-1	Sequence 1, Appli
26	37.5	43.1	154	2	US-08-911-434A-4	Sequence 4, Appli
27	37	42.5	157	4	US-09-215-221-20	Sequence 20, Appl
28	37	42.5	157	4	US-09-215-221-21	Sequence 21, Appl
29	37	42.5	558	4	US-09-146-080-2	Sequence 2, Appli
30	36	41.4	412	2	US-08-463-061B-14	Sequence 14, Appl
31	36	41.4	412	2	US-08-461-479A-14	Sequence 14, Appl
32	36	41.4	412	2	US-08-462-906B-14	Sequence 14, Appl
33	36	41.4	412	3	US-08-463-074B-14	Sequence 14, Appl
34	36	41.4	412	3	US-08-465-985C-14	Sequence 14, Appl
35	36	41.4	412	3	US-08-652-446-14	Sequence 14, Appl
36	36	41.4	440	1	US-07-637-870-8	Sequence 8, Appli
37	36	41.4	440	1	US-07-637-999-5	Sequence 5, Appli
38	36	41.4	440	1	US-08-112-208-5	Sequence 5, Appli
39	36	41.4	478	2	US-08-185-828A-17	Sequence 17, Appl
40	36	41.4	478	2	US-08-185-828A-20	Sequence 20, Appl
41	36	41.4	478	2	US-08-185-828A-23	Sequence 23, Appl
42	36	41.4	526	1	US-08-390-986B-4	Sequence 4, Appli
43	36	41.4	526	2	US-08-493-754A-4	Sequence 4, Appli
44	36	41.4	838	2	US-08-696-944-19	Sequence 19, Appl
45	35	40.2	153	1	US-08-469-486-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-08-795-430-9
; Sequence 9, Application US/08795430
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Altiatlo, Kati
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/023,871
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,182
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,611
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 40,153
; REFERENCE/DOCKET NUMBER: [illegible]
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300

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;       TELEFAX:  412/474 0448
;       TELEX:  25 3856
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-276-430-4


  Query Match             98.9%;  Score 86;  DB 4;  Length 17;
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
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Db       1 EEIIKFAAAHYNIEILK 17


RESULT   2
US-08-276-430-5
; Sequence 5, Application US/08276430
; Patent No. 6136771
; GENERAL INFORMATION:
;     APPLICANT:  Alitalo, Kari
;     APPLICANT:  Joukov, Vladimir
;     TITLE OF INVENTION:  Vascular Endothelial Growth Factor C (VEGF-C)
;     TITLE OF INVENTION:  Protein and Gene, Mutants Thereof, and Uses Thereof
;     NUMBER OF SEQUENCES:  57
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  United States of America
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  08/276,430
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/FI95/00427
;       FILING DATE:  01-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/671,573
;       FILING DATE:  28-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/601,132
;       FILING DATE:  14-FEB-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/585,895
;       FILING DATE:  12-JAN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/510,133
;       FILING DATE:  01-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/340,011
;       FILING DATE:  14-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Case, David A.
;       REGISTRATION NUMBER:  08,153
;       REFERENCE/DOCKET NUMBER:  2895/33691
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/474 6300
;       TELEFAX:  312/474 0448
;       TELEX:  25 3856
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  18 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-276-430-5


  Query Match             98.9%;  Score 86;  DB 4;  Length 18;
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  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
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Db       2 EEIIKFAAAHYNIEILK 18


RESULT   3
US-08-510-133A-13
; Sequence 13, Application US/08510133A
; Patent No. 5525639
;   GENERAL INFORMATION:
;       APPLICANT: Alitalo, Kari
;                  Joukov, Vladimir
;       TITLE OF INVENTION: Receptor Ligand
;       NUMBER OF SEQUENCES: 45
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: United States of America
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: 08/510,133A
;            FILING DATE: 01-Aug-1995
;            CLASSIFICATION: Unknown
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Case, David A.
;            REGISTRATION NUMBER: 08,153
;            REFERENCE/DOCKET NUMBER: 2811/33691
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/474 6300
;            TELEFAX: 312/474 0448
;            TELEX: 25 3856
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-510-133A-13


  Query Match             98.9%;  Score 86;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
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Db       2 EEIIKFAAAHYNIEILK 18


RESULT   4
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US-09-534-376A-5
; Sequence 15, Application US/09534376A
; Patent No. 6245538
; GENERAL INFORMATION:
;     APPLICANT: Alitalo, Kari
;     APPLICANT: Jeltsch, Vladimir
;     TITLE OF INVENTION: Receptor Ligand
;     NUMBER OF SEQUENCES: 45
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET: 6300 Sears Tower, 233 South Wacker Drive
;       CITY: Chicago
;       STATE: Illinois
;       COUNTRY: United States of America
;       ZIP: 60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/585,895
;       FILING DATE:
;       CLASSIFICATION: 514
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Cass, David A.
;       REGISTRATION NUMBER: 28,158
;       REFERENCE/DOCKET NUMBER: 2411/44972
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 312/474-6600
;       TELEFAX: 312/474-0448
;       TELEX: 25-3856
;   INFORMATION FOR SEQ ID NO: 15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 18 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-585-895-15


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Qy       2 EEIIKFAAAHYNIEILK 18
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Db       2 EEIIKFAAAHYNIEILK 18


RESULT   5
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5962540
; GENERAL INFORMATION:
;     APPLICANT: BU, JING SHAN
;     APPLICANT: ROSEN, CRAIG A.
;     APPLICANT: CAO, LIANG
;     TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;     NUMBER OF SEQUENCES: 15
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;       STREET: 1100 NEW YORK AVENUE
;       CITY: WASHINGTON
;       STATE: DC
;       COUNTRY: USA
;       ZIP: 20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/ 8/999,811
;       FILING DATE: HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/207,550
;       FILING DATE: 8 MAR 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 08/465,968
;       FILING DATE: 05 JUN 1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME: MARKWICK, KAREN R.
;       REGISTRATION NUMBER: 33,851
;       REFERENCE/DOCKET NUMBER: 1488.1000004
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202)371 2600
;       TELEFAX: (202)371 2540
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 350 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: linear
;     MOLECULE TYPE: protein
US-08-999-811-4


  Query Match             98.9%;  Score 86;  DB 2;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           |||||||||||||||||
Db      34 EEIIKFAAAHYNIEILK 50


RESULT   6
US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820
; GENERAL INFORMATION:
;  APPLICANT: Bu, Jing Shan
;  APPLICANT: Rosen, Craig A.
;  APPLICANT: Cao, Liang
;  TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
;  TITLE OF INVENTION: Factor 2
;  FILE REFERENCE: PF1120I
;  CURRENT APPLICATION NUMBER: US/08/824,996B
;  CURRENT FILING DATE: 1997-03-27
;  EARLIER APPLICATION NUMBER: 08/207,550
;  EARLIER FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-08-824-996-2


  Query Match             98.9%;  Score 86;  DB 2;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           |||||||||||||||||
Db      34 EEIIKFAAAHYNIEILK 50


RESULT   7
US-09-042-105-4
; Sequence 4, Application US/09042105
; Patent No. 6040157
;  GENERAL INFORMATION:
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;     APPLICANT:  HU, YING CHAN
;     APPLICANT:  FoSEN, CRAIG A.
;     APPLICANT:  CAO, LIANG
;     TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;     NUMBER OF SEQUENCES:  5
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX
;       STREET:  1100 NEW YORK AVENUE
;       CITY:  WASHINGTON
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/942,197
;       FILING DATE:  HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/207,550
;       FILING DATE:  8 MAR 1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/465,008
;       FILING DATE:  06 JUN 1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  To BE ASSIGNED
;       FILING DATE:  24 DEC 1997
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  ERIC K. STEFFE
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1888.[illegible]/EKS
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)371 2600
;       TELEFAX:  (202)371 2540
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  350 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-942-197-4


  Query Match              98.9%;  Score 86;  DB 3;  Length 350;
  Best Local Similarity   100.0%;  Prob. No. 1.5e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAARYNEELK 18
           ||||||||||||||||||
Db      45 EELIKEAAARYNEELK 61


RESULT  8
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent No. 6228839
;   GENERAL INFORMATION:
;       APPLICANT: Alitalo, Kari
;                  Isakov, Vladimir
;       TITLE OF INVENTION: Receptor Ligand
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: United States of America
;            ZIP: [illegible]-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC DOS/MS DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/510,133A
;            FILING DATE: 01 Aug 1995
;            CLASSIFICATION: Unknown
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Gass, David A.
;            REGISTRATION NUMBER: 38,153
;            REFERENCE/DOCKET NUMBER: 2811/33063
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/474 6300
;            TELEFAX: 312/474 0448
;            TELEX: 25 3856
;    INFORMATION FOR SEQ ID NO: 33:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 350 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33


  Query Match              98.9%;  Score 86;  DB 4;  Length 350;
  Best Local Similarity   100.0%;  Prob. No. 1.5e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAARYNEELK 18
           ||||||||||||||||||
Db      45 EELIKEAAARYNEELK 61


RESULT  9
US-08-485-865-33
; Sequence 33, Application US/08485865
; Patent No. 6245530
;  GENERAL INFORMATION:
;    APPLICANT:  Alitalo, Kari
;    APPLICANT:  Isakov, Vladimir
;    TITLE OF INVENTION:  Receptor Ligand
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,865
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gass, David A.
;      REGISTRATION NUMBER:  38,153
;      REFERENCE/DOCKET NUMBER:  2811/33072
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474 6300
;      TELEFAX:  312/474 0448
;      TELEX:  25 3856
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  350 amino acids
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;       TYPE:  amino acid
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-534-376A-5

  Query Match             98.9%;  Score 86;  DB 4;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
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Db     436 EEIIKFAAAHYNIEILK 452


RESULT  10
US-08-999-811-2
; Sequence 2, Application US/08999811
; Patent No. 5932540
;  GENERAL INFORMATION:
;    APPLICANT:  HU, JING SHAN
;    APPLICANT:  ROSEN, CRAIG A.
;    APPLICANT:  CAO, LIANG
;    TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY, AUSTIN, BROWN & WOOD
;      STREET:  1100 NEW YORK AVENUE
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/999,811
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,535
;      FILING DATE:  4-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/475,998
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MARKOWICZ, KAREN K.
;      REGISTRATION NUMBER:  35,951
;      REFERENCE/DOCKET NUMBER:  13995.1000004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)371-2600
;      TELEFAX:  (202)371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-999-811-2

  Query Match             98.9%;  Score 86;  DB 2;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           |||||||||||||||||
Db     134 EEIIKFAAAHYNIEILK 120


RESULT  11
US-09-042-105-2
; Sequence 2, Application US/09042105
; Patent No. 6041152
;  GENERAL INFORMATION:
;    APPLICANT:  HU, JING SHAN
;    APPLICANT:  ROSEN, CRAIG A.
;    APPLICANT:  CAO, LIANG
;    TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY, AUSTIN, BROWN & WOOD
;      STREET:  1100 NEW YORK AVENUE
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,105
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,535
;      FILING DATE:  4 MAR 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/465,998
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US TO BE ASSIGNED
;      FILING DATE:  24 DEC 1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERIC K. STEFFE
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  13995.1000004/EKS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)371 2600
;      TELEFAX:  (202)371 2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-042-105-2

  Query Match             98.9%;  Score 86;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEILK 18
           |||||||||||||||||
Db     104 EEIIKFAAAHYNIEILK 120


RESULT  12
US-09-042-105-18
; Sequence 18, Application US/09042105
; Patent No. 6041152
;  GENERAL INFORMATION:
;    APPLICANT:  HU, JING SHAN
;    APPLICANT:  ROSEN, CRAIG A.
;    APPLICANT:  CAO, LIANG
;    TITLE OF INVENTION:  VASCULAR ENDOTHELIAL GROWTH FACTOR 2
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  SIDNEY, KENNEDY, GOLDSTEIN & FOX
;       STREET:  1100 NEW YORK AVENUE
;       CITY:  WASHINGTON
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/042,105
;       FILING DATE:  HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/207,550
;       FILING DATE:  8 MAR 1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/065,068
;       FILING DATE:  06 JUN 1993
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  TO BE ASSIGNED
;       FILING DATE:  24 DEC 1992
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  ERIC K. STEFFE
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  CRW 2.0-032/PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)371 2600
;       TELEFAX:  (202)371 2540
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  419 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-042,105-18


  Query Match              98.0%;  Score 86;  DB 4;  Length 419;
  Best Local Similarity    100.0%;  Pred. No. 1.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAAHYNIELIK 18
           ||||||||||||||||||
Db     104 EELIKEAAAHYNIELIK 120


RESULT  13
US-08-295,440-8
; Sequence 8, Application US/08295440
; Patent No. 6140071
;   GENERAL INFORMATION:
;     APPLICANT:  Alitalo, Kari
;     APPLICANT:  Joukov, Vladimir
;     TITLE OF INVENTION:  Vascular Endothelial Growth Factor C (VEGF-C)
;     TITLE OF INVENTION:  Proteins and Genes, Mutants thereof, and Uses Thereof
;     NUMBER OF SEQUENCES:  57
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  United States of America
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/295,440
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/FI96/000427
;       FILING DATE:  01 AUG 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/671,573
;       FILING DATE:  28 JUN 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/601,132
;       FILING DATE:  14 FEB 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/585,895
;       FILING DATE:  12 JAN 1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/510,143
;       FILING DATE:  01 AUG 1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/340,011
;       FILING DATE:  14 NOV 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Cass, David A.
;       REGISTRATION NUMBER:  36,153
;       REFERENCE/DOCKET NUMBER:  2258.1/33601
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/474 6300
;       TELEFAX:  312/474 0448
;       TELEX:  25 3856
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  419 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-295,440-8


  Query Match              98.0%;  Score 86;  DB 4;  Length 419;
  Best Local Similarity    100.0%;  Pred. No. 1.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAAHYNIELIK 18
           ||||||||||||||||||
Db     104 EELIKEAAAHYNIELIK 120


RESULT  14
US-08-510,143A-5
; Sequence 5, Application US/08510143A
; Patent No. 5652349
;   GENERAL INFORMATION:
;       APPLICANT:  Alitalo, Kari
;                   Joukov, Vladimir
;       TITLE OF INVENTION:  Receptor Ligand
;       NUMBER OF SEQUENCES:  5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET:  6300 Sears Tower, 233 South Wacker Drive
;            CITY:  Chicago
;            STATE:  Illinois
;            COUNTRY:  United States of America
;            ZIP:  60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE:  Floppy disk
;            COMPUTER:  IBM PC compatible
;            OPERATING SYSTEM:  PC DOS/MS DOS
;            SOFTWARE:  PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER:  US/08/510,143A
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;              FILING DATE: 01-Aug-1995
;              CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;              NAME: Gass, David A.
;              REGISTRATION NUMBER: 36,153
;              REFERENCE/DOCKET NUMBER: 2811/32003
;        TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 312/474-6300
;              TELEFAX: 312/474-0448
;              TELEX: 25-3856
;    INFORMATION FOR SEQ ID NO: 45:
;        SEQUENCE CHARACTERISTICS:
;              LENGTH: 419 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-534-376A-45

  Query Match             98.9%;  Score 86;  DB 4;  Length 419;
  Best Local Similarity   100.0%;  Prod. No. 1.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LEPIKPAAAHYNPEILK 18
           ||||||||||||||||||
Db     134 LEPIKPAAAHYNPEILK 120


RESULT 15
PCT/US96/09001-2
; Sequence 2, Application PC/US9609001
;  GENERAL INFORMATION:
;    APPLICANT:  HOL, ET AL.
;    TITLE OF INVENTION:  Human Vascular Endothelial Growth Factor 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART &  OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09001
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/465,976
;      FILING DATE:  6-JUN-95
;      APPLICATION NUMBER:  08/207,550
;      FILING DATE:  8-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  225800-288
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
PCT/US96/09001-2

  Query Match             98.9%;  Score 86;  DB 5;  Length 419;
  Best Local Similarity   100.0%;  Prod. No. 1.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 LEPIKPAAAHYNPEILK 18
           ||||||||||||||||||
Db     134 LEPIKPAAAHYNPEILK 120


Search completed: February 22, 2002, 15:37:09
Job time: 152 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

M pi Test: protein search, using sw model

Run on: February 22, 2002, 15:31:27 ; Search time 23.76 Seconds
(without alignments)
*** Mill n Cell Updates/Sec

Title: US-09-534-376A-5
Perfect score: 867
Sequence: 1 XEEEIKEAAAHYNIEILK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /*****/*/data/p*****/p*****/*****.*
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13: /*****/*/data/p*****/p*****/*****.*
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18: /*****/*/data/p*****/p*****/*****.*
19: /*****/*/data/p*****/p*****/*****.*
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21: /*****/*/data/p*****/p*****/*****.*
22: /*****/*/data/p*****/p*****/AA*****.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	98.9	17	19	AAW75741	Human vascular end
2	86	98.9	18	19	AAW75738	FLT4 ligand N-term
3	86	98.9	113	20	AAY08285	Human VEGF-C wit fact
4	86	98.9	418	20	AAY08284	Human VEGF-C wit fact
5	86	98.9	450	20	AAY30519	A disintegrated vascul
6	86	98.9	450	20	AAY22421	Disintegrin human VE
7	86	98.9	450	21	AAY97145	Isolated vascular
8	86	98.9	450	22	AAY97577	Human VEGF-C protei
9	86	98.9	899	20	AAW86237	Human VEGF-C full
10	86	98.9	419	18	AAW17837	Human C-terminal fibri
11	86	98.9	419	18	AAW00932	Human FLT4 recepto
12	86	98.9	419	18	AAW11478	Human vascular end
13	86	98.9	419	19	AAW75751	Vascular endothelia
14	86	98.9	419	19	AAW75740	Human vascular end
15	86	98.9	419	20	AAY30518	Vascular endothelia
16	86	98.9	419	20	AAY22420	Full length human
17	86	98.9	419	20	AAW86235	Human vascular end
18	86	98.9	419	21	AAB10648	Human VEGF protein
19	86	98.9	419	21	AAB29048	Human VEGF-C prote
20	86	98.9	419	21	AAY97144	Vascular endothelia
21	86	98.9	419	21	AAY70749	Human proprotein vasc
22	86	98.9	419	21	AAY70982	Human vascular end
23	86	98.9	419	22	AAY97570	Human VEGF-C prote
24	86	98.9	419	22	AAB87666	Human VEGF-C, Hom
25	81	93.1	450	16	AAB62689	Vascular endothelia
26	77	88.5	419	18	AAW13833	Human vascular end
27	73	83.9	415	18	AAW00933	Mouse FLT4 recepto
28	73	83.9	415	19	AAW75742	Mouse vascular end
29	69	79.3	418	18	AAW00934	Quail FLT4 recepto
30	69	79.3	418	19	AAW75743	Quail vascular end
31	44	50.6	307	20	AAW86222	Human VEGF-C fragme
32	42.5	48.4	463	22	AAB92902	Human protein Seq
33	42.5	48.4	463	22	AAB94245	Human protein Seq
34	42.5	48.4	473	22	AAB62009	Human secreted pr
35	42	48.4	106	21	AAY08078	Cys2E protein whic
36	41	47.1	178	20	AAY08287	Human growth fact
37	41	47.1	321	19	AAW54243	Mus musculus vasc
38	41	47.1	326	19	AAW44299	Rat vascular endo
39	41	47.1	387	20	AAY08286	Human orf w2h fam
40	41	47.1	458	18	AAW14992	Murine c-Fos induc
41	41	47.1	458	19	AAW54242	Mus musculus vasc
42	41	47.1	458	19	AAW44296	Mouse vascular end
43	41	47.1	502	19	AAW34567	Thermotoga maritim
44	41	47.1	502	19	AAW49871	Thermotoga maritim
45	40	46.0	207	20	AAB41207	Soybean ubiquitin

ALIGNMENTS

RESULT 1
AAW75741
ID AAW75741 standard; peptide; 18 AA.
XX
AC AAW75741;
XX
DT 14-DEC-1998 (first entry)
XX
DE Human vascular endothelial growth factor peptide VEM 18.
XX
KW FLT4 receptor ligand; vascular endothelial cell;
KW lymphangiogenesis; angiogenesis; inflammation;
KW lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS Homo sapiens.
XX
PN WO9833917-A1.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-US01973.
XX
PR 05-FEB-1997; 97US-0794*.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Alitalo K, Jeltkov V;
XX
DR WPI; 1998-437470/37.
XX
PT New isolated vascular endothelial growth factor polypeptide(s)
PT used to develop products for treating, e.g. cancers, inflammation,
PT oedema, granulocyte penia or for wound healing or tissue

PT Transplantation
XX
PN Example 19; Page 50; 177pp; English.
XX
CC The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC activities affecting growth and migration of vascular endothelial cells,
CC promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC increasing vascular permeability, and affecting myelopoiesis. The
CC products can be used for stimulating angiogeneses, for inhibiting
CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC They can also be used for modulating the growth of endothelial cells.
CC They can also be used to stimulate lymphocyte production and maturation,
CC and to promote or inhibit trafficking of leucocytes between tissues and
CC lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ Sequence 17 AA;

Query Match 98.9%; Score 86; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EELIKFAAAHYNIELTLK 18
|||||||||||||||||
Db 1 eelikfaaahynieltlk 17

RESULT 2
AAW75748
ID AAW75748 standard; peptide; 18 AA.
XX
AC AAW75748;
XX
DT 14-DEC-1998 (first entry)
XX
DE FIIA ligand N-terminal amino acid sequence.
XX
KW FIIA; vascular endothelial growth factor C; vascular endothelial cell;
KW lymphatic endothelial cell; myelopoiesis; angiogenesis; inflammation;
KW lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Xaa is unspecified"
XX
PN WO9840017-A1.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-US001973.
XX
PR 05-FEB-1997; 97US-0037543P.
XX
PA (CORA-) CORIXA CORP.
PA (UYBP-) UNIV HELSINKI LICENSING LTD.
XX
PI Alitalo K; Lakso V;
XX
DR WPI; 1998-481747/41.
XX
PT New isolated vascular endothelial growth factor polypeptide(s)
PT used to develop products for treating, e.g. cancers, oedema, a
PT oedema, granulocytopenia or for wound healing or tissue
PT transplantation
XX
PS Example 5; Page 47; 177pp; English.
XX
CC The FIIA ligand polypeptide is an example of a vascular endothelial
CC growth factor C (VEGF-C). The VEGF-C polypeptides have activities
CC affecting growth and migration of vascular endothelial cells, promoting
CC growth of lymphatic endothelial cells and lymphatic vessels, increasing
CC vascular permeability, and affecting myelopoiesis. The products can be
CC used for stimulating angiogeneses, for inhibiting angiogenesis, for
CC stimulating lymphangiogenesis, treatment or prevention of inflammation,
CC oedema, elephantiasis, or Milroy's disease. They can also be used to
CC modulate myelopoiesis, e.g. treating granulocytopenia. They can also be
CC used for modulating the growth of endothelial cells. They can also be
CC used to stimulate lymphocyte production and maturation, and to promote or
CC inhibit trafficking of leucocytes between tissues and lymphatic vessels
CC or to affect migration in and out of the thymus.
XX
SQ Sequence 18 AA;

Query Match 98.9%; Score 86; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EELIKFAAAHYNIELTLK 18
|||||||||||||||||
Db 2 eelikfaaahynielTlk 18

RESULT 3
AAY08295
ID AAY08295 standard; Protein; 113 AA.
XX
AC AAY08295;
XX
DT 14-JUL-1999 (first entry)
XX
DE Human growth factor protein fragment VEGF-C113.
XX
KW Growth factor; human; dimer; cystein knot; cellular inclusion body;
KW pharmaceutical.
XX
OS Homo sapiens.
XX
PN DE19734734-A1.
XX
PD 04-MAY-1999.
XX
PF 05-NOV-1997; 97DE-1034734.
XX
PR 05-NOV-1997; 97DE-1034734.
XX
PA (GBHE-) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI Erdmann H; Kaerst U; Mueller C; Rinas U; Welch B;
XX
DR WPI; 1999-278785/24.
XX
PT Preparing active growth factor dimers from inclusion bodies in high
PT yield
XX
PS Claim 14; Page 8-9; 14pp; German.
XX
CC This invention describes the novel preparation of biologically active
CC dimers of recombinant human growth factors of the cysteine knot family
CC starting from cellular inclusion bodies. Such dimers are are useful in
CC pharmaceutical compositions and the method provides yields of 5-50%,
CC in examples, compared with about 1% for the conventional refold (see
CC Biochemistry, 28 (1989) 2950). AAY08276-Y08301 are human growth factor
CC protein fragments used in the method of the invention.
XX
SQ Sequence 113 AA;

Query Match 98.9%; Score 86; DB 20; Length 113;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 EEIIKFAAABYNIEILK 18
           |:|:|||||||||||||
Db       3 eeiiktaaabynteilk 19


RESULT   4
AAY98284
ID   AAY98284 standard; Protein; 418 AA.
XX
AC   AAY98284;
XX
DT   14-JUL-1999  (first entry)
XX
DE   Human growth factor protein fragment VEGF-2.
XX
KW   Growth factor; human; dimer; cystoine knot; cellular inclusion body;
KW   pharmaceutical.
XX
OS   Homo sapiens.
XX
PN   EP0748734 A1.
XX
PD   06-MAY-1999.
XX
PF   05-NOV-1997;   97IE-1048734.
XX
PR   05-NOV-1997;   97IE-1048734.
XX
PA   (GBEB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
PI   Erdmann H;  Knerst U;  Mueller C;  Rinas U;  Welch H;
XX
DR   WPI; 1999-278785/24.
XX
PT   Preparing active growth factor dimers from inclusion bodies in bio-
PT   yield
XX
PS   Claim 14; Page 8; 14pp; German.
XX
CC   This invention describes the novel preparation of biologically active
CC   dimers of recombinant human growth factors of the cystoine knot family
CC   starting from cellular inclusion bodies. Such dimers are are useful in
CC   pharmaceutical compositions and the method provides yields of 51 vs.7%
CC   in examples, compared with about 20% in the most advanced prior art (see
CC   Biochemistry, 28 (1989) 2955). AAY98278-AY98291 are human growth factor
CC   protein fragments used in the method of the invention.
XX
SQ   Sequence   418 AA;


  Query Match             98.9%;  Score 86;  DB 20;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAABYNIEILK 18
           |||||||||||||||||
Db       3 eeiiktaaabynteilk 19


RESULT   5
AAY30519
ID   AAY30519 standard; Protein; 450 AA.
XX
AC   AAY30519;
XX
DT   16-NOV-1999  (first entry)
XX
DE   A truncated vascular endothelial growth factor-2.
XX
KW   Human vascular endothelial growth factor-2; VEGF-2;
KW   vascular endothelial cell growth; endothelial cell mitogen; a;
KW   angiogenesis; blood pressure; blood flow; immune system disorder;
KW   immune cell; cancer; autoimmune disorder; blood protein disorder;
KW   ataxia telangiectasia; common variable immunodeficiency;
KW   Dyscrasia syndrome; HIV infection; HTLV-BLV infection;
KW   leukocyte adhesion deficiency syndrome; lymphopenia;
KW   phagocyte bactericidal dysfunction; severe combined immunodeficiency;
KW   Wiskott Aldrich disorder; anemia; thrombocytopenia; hemoglobinuria;
KW   allergy; asthma; allergic asthma.
XX
OS   Homo sapiens.
XX
PN   WO9940934 A1.
XX
PD   19-SEP-1999.
XX
PF   10-MAR-1999;   99WO-US005021.
XX
PR   13-MAR-1998;   98US-0042105.
PR   30-JUN-1998;   98US-0107997.
XX
PA   (HUMA ) HUMAN GENOME SCI INC.
XX
PI   Rosen CA;  Ruben SM;  Li Y;
XX
DR   WPI; 1999-551399/46.
DR   N-PSDB; AAZ10524.
XX
PT   New human vascular endothelial growth factor 2, used for treating card
PT   immune disorders and cancers
XX
PS   Example 2; Fig 2A; 222pp; English.
XX
CC   The present sequence represents a truncated, biologically active form
CC   of human vascular endothelial growth factor 2 (VEGF 2). The VEGF 2
CC   polypeptides have activities similar to VEGF. The VEGF 2 polypeptides
CC   stimulate the growth of vascular endothelial cells, stimulate endothelial
CC   cell migration, stimulate angiogenesis, decrease blood pressure, and
CC   increase blood flow. The polynucleotides and polypeptides can be used
CC   for preventing, treating or ameliorating a medical condition. The
CC   VEGF-2 polypeptides or polynucleotides may be useful in treating
CC   deficiencies or disorders of the immune system, by activating or
CC   inhibiting the proliferation, differentiation, or mobilization
CC   (chemotaxis) of immune cells. The etiology of these immune deficiencies
CC   or disorders may be genetic, somatic, such as cancer or some autoimmune
CC   disorders, acquired (e.g., by chemotherapy or toxins), or infections.
CC   Examples of immune deficiency syndromes include blood protein
CC   disorders, ataxia telangiectasia, common variable immunodeficiency,
CC   Dyscrasia syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion
CC   deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction,
CC   severe combined immunodeficiency (SCIDs), Wiskott Aldrich disorder,
CC   anemia, thrombocytopenia, or hemoglobinuria. They can also be used to
CC   modulate hemostatic or thrombolytic activity. Similarly allergic reactions
CC   and conditions such as asthma (particularly allergic asthma) or other
CC   respiratory problems, may also be treated.
XX
SQ   Sequence   450 AA;


  Query Match             98.9%;  Score 86;  DB 20;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAABYNIEILK 18
           |||||||||||||||||
Db      35 eeiiktaaabynteilk 51


RESULT   6
AAY22321
ID   AAY22321 standard; Protein; 550 AA.
XX
AC   AAY22321;
XX
DT   22-SEP-1999  (first entry)
XX
```

```
DE   Truncated human VEGF2 protein sequence.
XX
KW   VEGF 2; vascular endothelial growth factor 2; angiogenesis; bone damage;
KW   endothelial cell proliferation; tissue damage; therapy.
XX
OS   Homo sapiens.
XX
PN   US5766940-A.
XX
PD   09 JUN 1998.
XX
PF   24 DEC 1997;   97US-0998811.
XX
PR   24 DEC 1996;   96US-0770811.
PR   08 MAR 1994;   94US-0207550.
PR   06 JUN 1995;   95US-0465006.
XX
PA   (HUMA ) HUMAN GENOME SCI INC.
XX
PI   Cao L;  Hu T;  Rosen CA;
XX
DR   WPI; 1998-341606/47.
DR   N-PSDB; AAX84808.
XX
PT   Vascular endothelial growth factor 2 for wound healing and vascular
PT   repair.
XX
PS   Claim 1; Fig 2; 47pp; English.
XX
CC   This sequence is the vascular endothelial growth factor 2 (VEGF2),
CC   of the invention. The isolated polypeptide is useful for stimulating
CC   angiogenesis, by promoting the proliferation of endothelial cells, for
CC   the treatment of a wound, or for the treatment of tissue or bone damage.
XX
SQ   Sequence   350 AA;


  Query Match             98.9%;  Score 86;  DB 20;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNTEILK 18
           |||||||||||||||||
Db     151 EEIIKFAAAHYNTEILK 167


RESULT   7
AAY97145
ID   AAY97145 standard; protein; 350 AA.
XX
AC   AAY97145;
XX
DT   22 DEC 2000  (first entry)
XX
DE   Truncated vascular endothelial growth factor 2 (VEGF 2).
XX
KW   Vascular endothelial growth factor 2; VEGF 2; retina; angiogenesis;
KW   treatment; injury; degeneration; photoreceptors; eye;
KW   amyloid streaks; retinitis; pigmentosa; human;
KW   age related macular degeneration; diabetic retinopathy.
XX
OS   Homo sapiens.
XX
PN   WO200045865-A1.
XX
PD   10 AUG 2000.
XX
PF   07 FEB 2000; 2000WO-US03047.
XX
PR   08 FEB 1999;   99US-0119139.
PR   12 FEB 1999;   99US-0119926.
PR   03 JUN 1999;   99US-0137706.
PR   22 DEC 1999;   99US-0171505.
XX
PA   (HUMA ) HUMAN GENOME SCI INC.
XX
PI   Rosen CA;  Alderson R;  Melder R;  Roschke V;  Ruben SM;
XX
DR   WPI; 2000-542862/48.
DR   N-PSDB; AAA52081.
XX
PT   Treating injury or degeneration of photoreceptors comprises
PT   administering to a subject vascular endothelial growth factor 2
PT   (VEGF 2)
XX
PS   Claim 4; Fig 2; 252pp; English.
XX
CC   Administration of vascular endothelial growth factor 2 (VEGF 2)
CC   to a patient can be used for treating injury or degeneration of
CC   photoreceptors associated with e.g. amyloid streaks, retinitis
CC   pigmentosa, age related macular degeneration, diabetic retinopathy,
CC   etc. VEGF 2 promotes angiogenesis, the formation of new blood
CC   vessels in the retina.
XX
SQ   Sequence   350 AA;


  Query Match             98.9%;  Score 86;  DB 21;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNTEILK 18
           |||||||||||||||||
Db     151 EEIIKFAAAHYNTEILK 167


RESULT   8
AAY97577
ID   AAY97577 standard; protein; 350 AA.
XX
AC   AAY97577;
XX
DT   05 APR 2001  (first entry)
XX
DE   Human VEGF 2 protein sequence.
XX
KW   Human; angiogenic protein; wound healing; vascular tissue repair;
KW   peripheral arterial disease; critical limb ischaemia; coronary disease;
KW   angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
KW   rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
KW   infectious disease; neurodegeneration;
KW   vascular endothelial growth factor 2; VEGF 2.
XX
OS   Homo sapiens.
XX
PN   WO200075163-A1.
XX
PD   14 DEC 2000.
XX
PF   01 JUN 2000; 2000WO-US14925.
XX
PR   03 JUN 1999;   99US-0137706.
XX
PA   (HUMA ) HUMAN GENOME SCI INC.
XX
PI   Rosen CA;  Ruben SM;  Hu T;  Cao L;
XX
DR   WPI; 2001-071057/08.
DR   N-PSDB; AAA96010.
XX
PT   New nucleic acid encoding angiogenic proteins, useful e.g. for
PT   promoting healing of wounds and treating peripheral arterial disease,
PT   critical limb ischaemia or coronary disease
XX
PS   Disclosure; Fig 2; 244pp; English.
XX
```

```
CC   This sequence is vascular endothelial growth factor 2 (VEGF-2),
CC   which is an angiogenic protein of the invention. The antibodies proteins
CC   and the DNA sequences encoding them, are used to prevent, treat or
CC   ameliorate disease and to detect diseases, or susceptibility, by
CC   detecting mutations or the presence or amount of angiogenic protein
CC   expression. Particularly they are used to stimulate wound healing,
CC   growth of damaged bone and tissue, and for repair of vascular tissue,
CC   especially peripheral arterial disease, critical limb ischaemia or
CC   coronary disease. Antagonists of the sequences are used to inhibit
CC   angiogenesis in tumours and to treat inflammation (where associated with
CC   increased vascular permeability), diabetic retinopathy, rheumatoid
CC   arthritis or psoriasis. Agonists are also useful for stimulating
CC   (lymph)angiogenesis. The proteins are also used to identify specific
CC   binding agents (potential therapeutic agents) and to raise antibodies.
CC   The antibodies are useful as therapeutic (ant)agonists; for detection,
CC   purification and targeting of proteins for in vivo or in vitro diagnosis
CC   (including imaging) or for therapy (including when linked to e.g. a label
CC   or cytotoxin), and for immunotyping of cells, e.g. for detecting minimal
CC   residual disease or haematopoietic progenitor/stem cells. It is also
CC   contemplated that the sequences might be useful for treating a body wide
CC   range of other disorders, e.g. autoimmune diseases; allergy; cancer;
CC   infectious diseases (viral, bacterial, fungal or parasitic);
CC   neurodegeneration, also as chemotactic agents or for stimulating
CC   regeneration of the nervous system etc.
XX
SQ   Sequence   450 AA;


  Query Match             98.9%;  Score 86;  DB 22;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAAHYNEEIGK 18
           |||||||||||||||||
Db      85 eelikeaaahyntgiik 51


RESULT  9
AAW86247
ID   AAW86247 standard; protein; 450 AA.
XX
AC   AAW86247;
XX
DT   15-FEB-1999  (first entry)
XX
DE   Human VEGF-2 full length sequence.
XX
KW   VEGF; VRP; vascular endothelial growth factor; VEGF related protein;
KW   recombinant; truncated; gene therapy; angiogenesis; cardiac ischaemia;
KW   coronary; collateral vessel development; cell growth; migration; heart;
KW   lower limb ischaemia; stroke; peripheral vascular disease; healing;
KW   wound healing; skin; vascular permeability.
XX
OS   Homo sapiens.
XX
PN   WO9844000-A2.
XX
PD   05-NOV-1998.
XX
PF   26-APR-1998;   98WO-US007851.
XX
PR   25-APR-1997;   97US-0842984.
XX
PA   (VICL ) VICAL INC.
XX
PI   Bohlen P;
XX
DR   WPI; 1999-009426/01.
XX
PT   New truncated vascular endothelial growth factor related (VEGF)
PT   subunits - lack part of the N terminal sequence, used to stimulate
PT   angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS   Claim 5; Fig 2b; 114pp; English.
XX
CC   The invention relates to truncated VRF (vascular endothelial growth
CC   factor (VEGF) related protein) subunits that have at least one amino
CC   acid N-terminal to the first Cys of the core sequence deleted. Host
CC   cells transformed or transfected with expression vectors containing
CC   nucleic acids encoding the truncated VRP subunits are used to produce
CC   the truncated proteins recombinantly. The truncated VRP subunits,
CC   optionally expressed from gene therapy vectors, have in vivo and in vitro
CC   angiogenic activity and are used to stimulate angiogenesis, particularly
CC   coronary collateral vessel development in cases of cardiac ischaemia; to
CC   stimulate endothelial cell growth and migration in vitro; to treat heart
CC   disease, to treat ischaemia (e.g. cardiac, chronic coronary or chronic
CC   lower limb ischaemia; stroke and peripheral vascular disease); to promote
CC   healing of wounds (of skin or intestines), and to increase vascular
CC   permeability. Sequences AAW86234 to AAW86239 represent full length VRF
CC   sequences from which the truncated fragments are created.
XX
SQ   Sequence   399 AA;


  Query Match             98.9%;  Score 86;  DB 20;  Length 399;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EELIKEAAAHYNEEIGK 18
           |||||||||||||||||
Db      84 eelikeaaahyntgiik 100


RESULT  10
AAW17847
ID   AAW17847 standard; protein; 419 AA.
XX
AC   AAW17847;
XX
DT   13-JAN-1998  (first entry)
XX
DE   Human foetal liver kinase A binding protein flk-1bp.
XX
KW   Foetal liver kinase 1 binding protein; human; flk 1bp;
KW   receptor tyrosine kinase; vasculogenesis; angiogenesis;
KW   wound healing; tumour; therapy; antagonist; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig peptide
FT   Protein         21..419
FT                   /label= Mat protein
FT                   /note= "(Claim 10)"
FT   Peptide         21..45
FT                   /label= N terminal
FT                   /note= "(Claim 9)"
XX
PN   WO9717442-A1.
XX
PD   15-MAY-1997.
XX
PF   05-NOV-1996;   96WO-US017584.
XX
PR   08-NOV-1995;   95US-0554324.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Lyman SD;
XX
DR   WPI; 1997-281031/25.
DR   N-PSDB; AAI68811.
XX
PT   DNA encoding a human foetal liver kinase 1 binding protein - used
PT   to treat conditions with insufficient protein, deliver agents to
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PT   cells and identify antagonists to treat protein mediated conditions.
XX
PN   Claim 1; Page 90-92; 43pp; English.
XX
CC   This polypeptide comprises a human foetal liver kinase 1 binding
CC   protein (flk 1bp) (see AAW17847) that binds to the receptor tyrosine
CC   kinase flk 1 expressed on vascular endothelial and other cells.
CC   The mature flk1 bp can be secreted from host cells transformed with
CC   an expression vector including an isolated flk 1bp cDNA clone (see
CC   AA168011).  Flk 1bp can be used to isolate cells to which it binds,
CC   for use in studying the roles of such cells and of flk 1 in
CC   vasculogenesis and angiogenesis.  Angiogenesis inhibitors or
CC   increased vascularisation may be clinically desirable (e.g. to
CC   suppress solid tumour growth or in wound healing, respectively).
CC   The flk 1bp can be administered to treat conditions with defective
CC   or insufficient flk 1.  Polypeptides may also act as vehicles to
CC   deliver diagnostic/therapeutic agents to cells to which flk1 bp
CC   binds, to generate antibodies, and to identify flk 1bp antagonists
CC   useful for treating flk 1bp mediated conditions.
XX
SQ   Sequence   419 AA;


  Query Match              98.9%;  Score 86;  DB 18;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEICKFAAAHYNIEILK 18
           |||||||||||||||||
Db     104 eeickfaaahynteilk 120


RESULT  11
AAW00942
ID   AAW00942 standard; Protein; 419 AA.
XX
AC   AAW00942;
XX
DT   10-NOV-1997  (first entry)
XX
DE   Human Flt4 receptor tyrosine kinase ligand VEGF C.
XX
KW   VEGF C; Flt4; receptor tyrosine kinase; VEGFR 3; human;
KW   vascular endothelial growth factor receptor 3; ligand;
KW   angiogenesis; wound healing; lymph vessel; lymphaticvas;
KW   cancer; metastasis; therapy; diagnosis; antibody; inhibitor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..102
FT                   /label= Prepro peptide
FT   Peptide         42..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 15)"
FT   Peptide         103..217
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 12)"
FT   Peptide         103..225
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 14)"
FT   Peptide         103..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 11)"
FT   Peptide         113..217
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 13)"
FT   Peptide         113..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 10)"
FT   Peptide         161..217
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 9)"
FT   Peptide         161..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 8)"
XX
PN   WO9727306-A2.
XX
PD   13-FEB-1997.
XX
PF   01-AUG-1996;   96WO-EP03427.
XX
PR   28-JUN-1996;   96US-0671572.
PR   01-AUG-1995;   95US-0510133.
PR   12-JAN-1996;   96US-0585895.
PR   14-FEB-1996;   96US-0601142.
XX
PA   (SYBE ) SYNTV BELGIENKI LICENSING LTD OY.
XX
PI   Alitalo K, Jeltsch V;
XX
DR   WPI; 1997-145508/13.
DR   N-PSDB; AAI84276.
XX
PT   Flt4 receptor tyrosine kinase ligand and related nucleic acid   used
PT   to modulate growth of endothelial cells and for diagnosis of
PT   endothelial cell diseases
XX
PS   Claim 7; Page 112-113; 183pp; English.
XX
CC   This polypeptide comprises the pre pro sequence of human VEGF C,
CC   a novel ligand that binds specifically to human Flt4 receptor
CC   tyrosine kinase (VEGFR 3), stimulating phosphorylation of the
CC   receptor.  Its sequence was deduced from a cDNA clone (AAI84276)
CC   obtd. from a PC 3 prostatic adenocarcinoma cell (ATCC CRL 1435)
CC   library.  The polypeptide, or its active fragments, can be
CC   expressed in transformed or transfected host cells for use in
CC   claimed methods for detecting endothelial cells (e.g. to image
CC   lymphatic vessels, endothelial venules, Flt4 receptor in
CC   histochemical tissue) and also to modulate the growth of mammalian
CC   endothelial cells (e.g. to accelerate angiogenesis and to promote
CC   endothelial function of lymphatic vessels).  Inhibitors of
CC   VEGF C, such as antibodies, can be used to control endothelial
CC   cell proliferation, e.g. lymphangioma or metastatic cancer.
CC   Mouse and quail VEGF C sequences (see AAW00944-45) have also been
CC   isolated.
XX
SQ   Sequence   419 AA;


  Query Match              98.9%;  Score 86;  DB 18;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEICKFAAAHYNIEILK 18
           |||||||||||||||||
Db     104 eeickfaaahynteilk 120


RESULT  12
AAW11478
ID   AAW11478 standard; Protein; 419 AA.
XX
AC   AAW11478;
XX
DT   23-APR-1997  (first entry)
XX
DE   Human vascular endothelial growth factor 2.
XX
KW   Vascular endothelial growth factor 2; VEGF2; angiogenesis;
KW   endothelialisation; coronary bypass surgery; vascular graft surgery;
KW   agonist; antagonist; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
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```
FH   Key             Location/Qualifiers
FT   Peptide         1..419
FT                   /label= Sig_peptide
FT   Protein         47..419
FT                   /label= Mat_protein
FT                   /note= "the mature protein is separated from the
FT                        (Claim 5)"
XX
PN   WO9833917-A1.
XX
PD   06-AUG-1998.
XX
PF   02-FEB-1998;    98WO-US001973.
XX
PR   05-FEB-1997;    97US-0037954P.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD.
XX
PI   Alitalo K, Jeltsch M, Lymboussaki A;
XX
DR   WPI; 1998-447479/38.
XX
PT   New isolated vascular endothelial growth factor polypeptide(s)
PT   used to develop products for treating, e.g. cancers, inflammation,
PT   oedema, granulocytopenia or for wound healing or tissue
PT   transplantation
XX
PS   Example 15; Page 143-145; 127pp; English.
XX
CC   The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC   activities affecting growth and migration of vascular endothelial cells,
CC   promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC   increasing vascular permeability, and affecting myelopoiesis. The
CC   products can be used for stimulating angiogeneses, for inhibiting
CC   angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC   of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC   also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC   They can also be used for modulating the growth of endothelial cells.
CC   They can also be used to stimulate lymphocyte production and maturation,
CC   and to promote or inhibit trafficking of lymphocytes between tissues and
CC   lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ   Sequence   419 AA;


  Query Match             98.9%;  Score 86;  DB 19;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKPAAAHYNIEILK 18
           ||||||||||||||||| |
Db     104 eeiikpaaahynteilk 120


RESULT  14
AAW75740
ID   AAW75740 standard; Protein; 419 AA.
XX
AC   AAW75740;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Human vascular endothelial growth factor C protein.
XX
KW   FLT4; vascular endothelial growth factor C; vascular endothelial cell...
KW   lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation;
KW   lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS   Homo sapiens.
XX
PN   WO9833917-A1.
XX
PD   06-AUG-1998.
XX
PF   02-FEB-1998;    98WO-US001973.
XX
PR   05-FEB-1997;    97US-0037954P.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD.
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XX
PN   Alitalo K,  Jeltsch, V,
XX
DR   WPI; 1998-137170/37
DR   N-PSDB; AAV52576.
XX
PT   New isolated vascular endothelial growth factor polypept.e(s)
PT   used to develop products for treating, e.g. cancers, inflammation,
PT   oedema, granulocytopenia or for wound healing or tissue
PT   transplantation
XX
PS   Claim 1; Page 112; 177pp; English.
XX
CC   The vascular endothelial growth factor C (VEGF C) polypeptides have
CC   activities affecting growth and migration of vascular endothelial cells,
CC   promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC   increasing vascular permeability, and affecting myelopoiesis. The
CC   products can be used for stimulating angiogeneses, for inhibiting
CC   angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC   of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC   also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC   They can also be used for modulating the growth of endothelial cells.
CC   They can also be used to stimulate lymphocyte proliferation and maturation,
CC   and to promote or inhibit trafficking of leucocytes between tissues and
CC   lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ   Sequence  419 AA;


  Query Match             98.9%;  Score 86;  DB 19;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEIIK 18
           |||||||||||||||||
Db     104 eeiikfaaahynieiik 120


RESULT  15
AAY40518
ID   AAY40518 standard; Protein; 419 AA.
XX
AC   AAY40518;
XX
DT   16-NOV-1999  (first entry)
XX
DE   Vascular endothelial growth factor 2 (VEGF 2).
XX
KW   Human vascular endothelial growth factor 2; VEGF 2;
KW   vascular endothelial cell growth; endothelial cell mitogen; ;
KW   angiogenesis; blood pressure; blood flow; immune system disorder;
KW   immune cell; cancer; autoimmune disorder; blood protein disorder;
KW   ataxia telangiectasia; common variable immunodeficiency;
KW   Di George syndrome; HIV infection; HTLV BLV infection;
KW   leukocyte adhesion deficiency syndrome; lymphopenia;
KW   phagocyte bactericidal dysfunction; severe combined immunodeficiency;
KW   Wiskott Aldrich disorder; anemia; thrombocytopenia; hemoglobinuria;
KW   allergy; asthma; allergic asthma.
XX
OS   Homo sapiens.
XX
PN   WO9946364-A1.
XX
PD   16-SEP-1999.
XX
PF   10-MAR-1999;   99WO-US005021.
XX
PR   13-MAR-1998;   98US-0042105.
PR   30-JUN-1998;   98US-0091007.
XX
PA   (HUMA ) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Wolf N;

XX
DR   WPI; 2000-552909/46.
DR   N-PSDB; AAZ10723.
XX
PT   New human vascular endothelial growth factor 2, used for treating, e.g.
PT   immune disorders and cancers
XX
PS   Claim 12; Fig 1A E; 222pp; English.
XX
CC   The present sequence represents vascular endothelial growth factor 2
CC   (VEGF 2). The VEGF 2 polypeptides have activities similar to VEGF. The
CC   VEGF 2 polypeptides stimulate the growth of vascular endothelial cells,
CC   stimulate endothelial cell migration, stimulate angiogenesis, decrease
CC   blood pressure, and increase blood flow. The polynucleotides and
CC   polypeptides can be used for preventing, treating or ameliorating a
CC   medical condition. The VEGF 2 polypeptides or polynucleotides may be
CC   useful in treating deficiencies or disorders of the immune system, by
CC   activating or inhibiting the proliferation, differentiation, or
CC   mobilization (chemotaxis) of immune cells. The etiology of these immune
CC   deficiencies or disorders may be genetic, somatic, such as cancer or
CC   some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or
CC   infectious. Examples of immunologic deficiency syndromes include blood
CC   protein disorders, ataxia telangiectasia, common variable
CC   immunodeficiency, Digeorge syndrome, HIV infection, HTLV BLV infection,
CC   leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte
CC   bactericidal dysfunction, severe combined immunodeficiency (SCIDs),
CC   Wiskott Aldrich disorder, anemia, thrombocytopenia, or hemoglobinuria.
CC   They can also be used to modulate emostatic or thrombolytic activity.
CC   Similarly allergic reactions and conditions such as asthma (particularly
CC   allergic asthma) or other respiratory problems, may also be treated.
XX
SQ   Sequence  419 AA;


  Query Match             98.9%;  Score 86;  DB 20;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 EEIIKFAAAHYNIEIIK 18
           |||||||||||||||||
Db     104 eeiikfaaahynieiik 120


Search completed: February 22, 2002, 15:46:50
Job time:  2.3 secs
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: February 22, 2002, 14:27:27 ; Search time 1.5 Seconds
(without alignments)
1101.991 Million cell updates/sec

Title: US-09-534-376A-11
Perfect score: 2383
Sequence: 1 MHLLGFLSLACSLIAAALIPKEAE.....SFSSFEVPKVESVAAESQGESAGFLWGVKAPPQKDLEPA 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Prot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. | Query Match | Score | Match Length | DB | ID | Description
1 | 87.8 | 2047.5 | 428 | 6 | Q9XS50 | Q9XS50 Bos taurus (
2 | 25.5 | 1762.5 | 418 | 13 | O57352 | O57352 Ovophis ok
3 | 29.8 | 696 | 354 | 4 | Q43915 | Q43915 Homo sapien
4 | 29.6 | 688.5 | 358 | 11 | Q92946 | Q92946 Rana boscai
5 | 29.5 | 686 | 126 | 11 | Q95Z97 | Q95Z97 Rattus norv
6 | 28.2 | 656.5 | 326 | 11 | Q95Z91 | Q95Z91 Rattus norv
7 | 11.8 | 274.5 | 1794 | 5 | Q64449 | Q64449 Mus musculus
8 | 11.1 | 260 | 1698 | 5 | Q04428 | Q04428 Mus musculus
9 | 9.9 | 231 | 232 | 4 | Q9BLW9 | Q9BLW9 Homo Sapiens
10 | 9.9 | 231 | 254 | 4 | Q16889 | Q16889 Homo Sapiens
11 | 9.5 | 222.5 | 214 | 6 | Q9MYV3 | Q9MYV3 Canis famil
12 | 9.5 | 221.5 | 208 | 6 | Q9XSF4 | Q9XSF4 Canis famil
13 | 9.4 | 219.5 | 209 | 4 | Q96T20 | Q96T20 Homo sapien
14 | 9.4 | 217.5 | 214 | 6 | Q9XSF5 | Q9XSF5 Canis famil
15 | 9.2 | 214.5 | 190 | 6 | Q9XSF3 | Q9XSF3 Canis famil
16 | 9.1 | 212.5 | 190 | 6 | Q9GKR0 | Q9GKR0 Equus cabal
17 | 8.9 | 208.5 | 198 | 6 | Q9GL52 | Q9GL52 Ovis aries
18 | 8.8 | 205 | 122 | 6 | Q9GLX1 | Q9GLX1 Bos taurus
19 | 8.7 | 203 | 194 | 13 | O42572 | O42572 Xenopus lae
20 | 8.6 | 199.5 | 134 | 4 | Q77443 | Q77443 Ovis aries
21 | 8.6 | 199.5 | 140 | 11 | Q9QX39 | Q9QX39 Spalax ehre
22 | 8.6 | 199.5 | 191 | 4 | O75876 | O75876 Homo sapien
23 | 8.4 | 196.5 | 214 | 11 | Q9QX07 | Q9QX07 Rattus norv
24 | 8.4 | 195 | 174 | 4 | Q6BL23 | Q6BL23 Homo sapien
25 | 8.2 | 191.5 | 190 | 11 | Q99ES2 | Q99ES2 Mesocricetu
26 | 8.1 | 188.5 | 188 | 13 | O73682 | O73682 Brachydani
27 | 8.1 | 188.5 | 314 | 5 | Q9BLX1 | Q9BLX1 Capra sphin
28 | 8.1 | 188.5 | 704 | 4 | O71567 | O71567 Trichoderma
29 | 8.0 | 187.5 | 171 | 4 | Q9BLW8 | Q9BLW8 Homo Sapien
30 | 7.9 | 184.5 | 147 | 4 | Q9BLP8 | Q9BLP8 Homo sapien
31 | 7.9 | 184 | 142 | 11 | Q9EBI6 | Q9EBI6 Mesocricetu
32 | 7.8 | 181.5 | 154 | 11 | O54881 | O54881 Rattus norv
33 | 7.7 | 180 | 124 | 6 | Q9XBC0 | Q9XBC0 Canis fix
34 | 7.7 | 180 | 301 | 5 | Q9VWP6 | Q9VWP6 Drosophila
35 | 7.7 | 179.5 | 148 | 13 | O42571 | O42571 Xenopus lae
36 | 7.7 | 179.5 | 196 | 6 | Q9XS48 | Q9XS48 Bos taurus
37 | 7.6 | 176.5 | 2452 | 5 | O61240 | O61240 Heliosynthia
38 | 7.5 | 176 | 126 | 6 | Q9BLE7 | Q9BLE7 Macaca mula
39 | 7.5 | 176 | 800 | 5 | Q9VB79 | Q9VB79 Drosophila
40 | 7.4 | 174.5 | 118 | 6 | Q9MZB8 | Q9MZB8 Ovis aries
41 | 7.4 | 172 | 2471 | 4 | Q04721 | Q04721 Homo sapien
42 | 7.4 | 172 | 2471 | 4 | Q9BZ40 | Q9BZ40 Homo sapien
43 | 7.4 | 171.5 | 170 | 11 | Q9QBX7 | Q9QBX7 Rattus norv
44 | 7.3 | 170 | 2471 | 11 | Q9QW30 | Q9QW30 Rattus sp.
45 | 7.3 | 169.5 | 146 | 11 | Q9QX56 | Q9QX56 Rattus norv

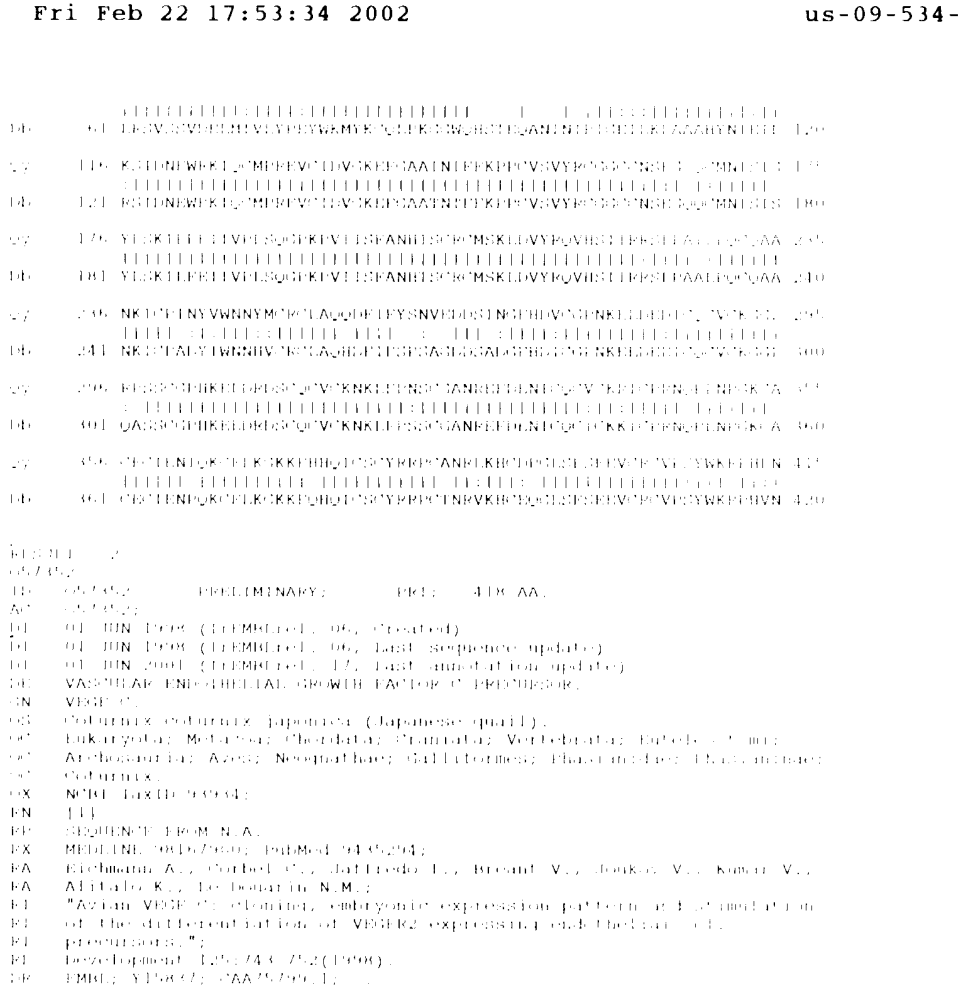
ALIGNMENTS

RESULT 1
Q9XS50
ID Q9XS50 PRELIMINARY; PRT; 428 AA.
AC Q9XS50;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Liu X., Yonekura H., Yamamoto S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB004275; BAA77087.1; -.
DR HSSP; P15692; 1VPF.
DR InterPro; IPR002072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001620; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 428 VASCULAR ENDOTHELIAL GROWTH FACTOR.
SQ SEQUENCE 428 AA; 46081 MW; 58BA84417A79E2D7 CRC64;

Query Match 87.8%; Score 2047.5; DB 6; Length 428;
Best Local Similarity 85.5%; Pred. No. 1.1e-186;
Matches 359; Conservative 27; Mismatches 29; Indels 5; Gaps 2;

Qy 1 MHLLGFLSLACSLIAAALIPKEAE-AIVAAFESGLDLSDAETAMIKSTVKAFPQKDLEPA 59
MHLLGFLSLACSLIAAALIPKEAE-AIVAAFESGLDLSDAETAMIKSTVKAFPQKDLEPA
Db 1 MHLLGFLSVACSLIAAALIPKEAEAIVAAAAAFESGLDLSDTETATIKENVKAYHGKEMDPA 60

Qy 60 TRSVSSVDFIMSVLYTDYWKMYKCQLRKGGWQE-QPTLNTEYQLSVKFEAAAHYNTEIL 118



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DE   Sequence 1PR000072; PLGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   354 AA;  40444 MW;  2048D7600735173E CRC64;


  Query Match             29.8%;  Score 696;  DB 4;  Length 354;
  Best Local Similarity   38.6%;  Pred. No. 1.2e-58;
  Matches  134;  Conservative   57;  Mismatches   96;  Indels   27;  Gaps   11;

Qy      42 CEVKAEDRDQL  EEQLRSVSCVFELMEVFPSYWKMYKGVLDKKDLVVYSGIKHMKMHV 101
           | ||:       |   |:|:|:| |:|:||: : : :|:|:|:|:|   :       : : |
Db      27 CPVERSSQQSLEERSPQQVIPAAASLEELLPITHSEDWKELWRCKELKSPINMLSLSASHKS 86

Qy     102 VEEAAARYNIELLPSTFDNFMEYLMMFEEYVPGNVKSALKEKFNEYIPLEKKATSRVDNGE 161
           :|||  |: | ||  |: |:|:|| ||| |:|:  | | :|||||||||:|:|| : |:|:|.
Db      87 IPIAAIFYSLETLLEVSGIGIDPWQFVESSLRVSVDLLLNTFEERIV-VNVEE : :|  130

Qy     162 NSEMLQMNISLGYLSKILDPEIIVPLSQGPKFVELSFANDITSCHGMSKLIVYRQVHSLIRGSLPA 221
           : : |||||| ||:| ||||:|:  |: | :  ||:| |:|:  |:|:|:|:|:|:|:|:|:|:|
Db     131 NDESLCFMNISLGYLSKFLEPEIIVPLSVPELVEVEVANNFSGCGLIAF  ePHEYSIIR 203

Qy     222 RSLPATLPQ   CQAANKICPTNYVWNNYMICRCLAQQHDFIFYSNVEIPSGINGTHEVVGPN 279
           ||:   :||   | : | ||  : :|:|  |:|: |          |:   :  |    :
Db     204 RSI  QTPEEDRCSHSKKLCFPIDMLWDSNKCKCVLQ  : : ::: eeNLLAYIIP---R 260

Qy     280 RKLCPTNYVWNNYMICRCLAQQHDFIFYSNVEIPSGINGTHEVVGPNKLLVEKQLL VCKVGL 339
           : ||  : :|:|  |:|: |          ::    :  |    :  | |
Db     261 RKLCPTDMEWENKCKCVLQ---  ---  DETPLPGIEL---  HSYIQE  :       : 299

Qy     340 RDFSSQGPHKELLNGSCQVVTRNKLFTNCCQANKETTERTCQCVCKKLDTCPNLIDNPCPKA 399
           : ||||                                  |||: |:|||  || :   :|  |:
Db     300 PTLCGPH  :          ::                MIEDEDRCECVCKAPCPSDLIQHPENCS 354

Qy     400 C EGTENTLKCTLTKDKKECRDPGLSFSFE 430
           | || :: :  | | |:  |::      : :|:|  |      : :|
Db     355 CPEGKESLESCKQKKIEHPDDCSCTIPCTFEHIRLCASKKPACCKHWKLKKI 410


RESULT   5
Q35757
ID   Q35757      PRELIMINARY;      PRT:   126 AA.
AC   Q35757;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   05-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN SPRAGUE-DAWLEY; TISSUE=LUNG;
RA   Mandriota S.J., Pepper M.S.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF010362; AAB63248.1; -.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     126     126
SQ   SEQUENCE   126 AA;  13927 MW;  8E365AFB0341D37B0 CRC64;


  Query Match             29.5%;  Score 689;  DB 11;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 5.8e-58;
  Matches  123;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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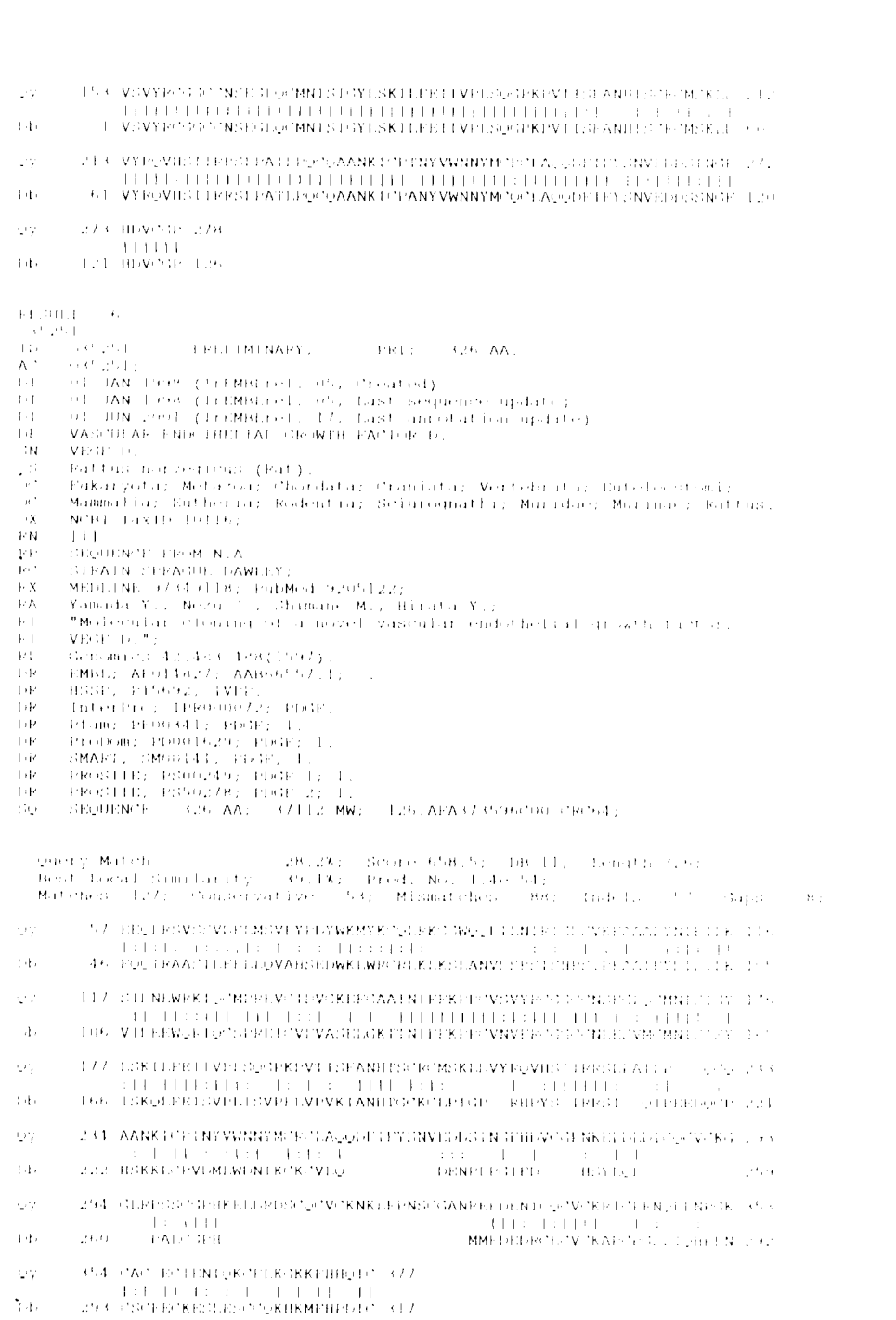


RESULT 1
Q94436
ID Q94436 PRELIMINARY; PRT; 1704 AA.
AC Q94436;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 220 KDA STICK PROTEIN.
GN SF220.
OS Chironomus thummi thummi (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomoidea; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7155;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Case S.L., Cox C., Bell W.J., Hoffman R.L., Martin J., Burch-Cox B.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U54431; AAA69804.1; -.
DR InterPro; IPR000561; EGF_like;
DR InterPro; IPR000084; Mu_thrombin_motif;
DR PRINTS; PR00076; MINEMAIoDE;
DR PROSITE; PS00022; EGF_1; UNKNOWN_2;
DR PROSITE; PS01186; EGF_2; UNKNOWN_1;
SQ SEQUENCE 1704 AA; 185745 MW; 4A4F2624A78FEE28 CRC64;

Query Match 11.8%; Score 274.5; DB 5; Length 1704;
Best Local Similarity 25.4%; Pred. No. 5.2e-17;
Matches 89; Conservative 41; Mismatches 132; Indels 70; Gaps 17;

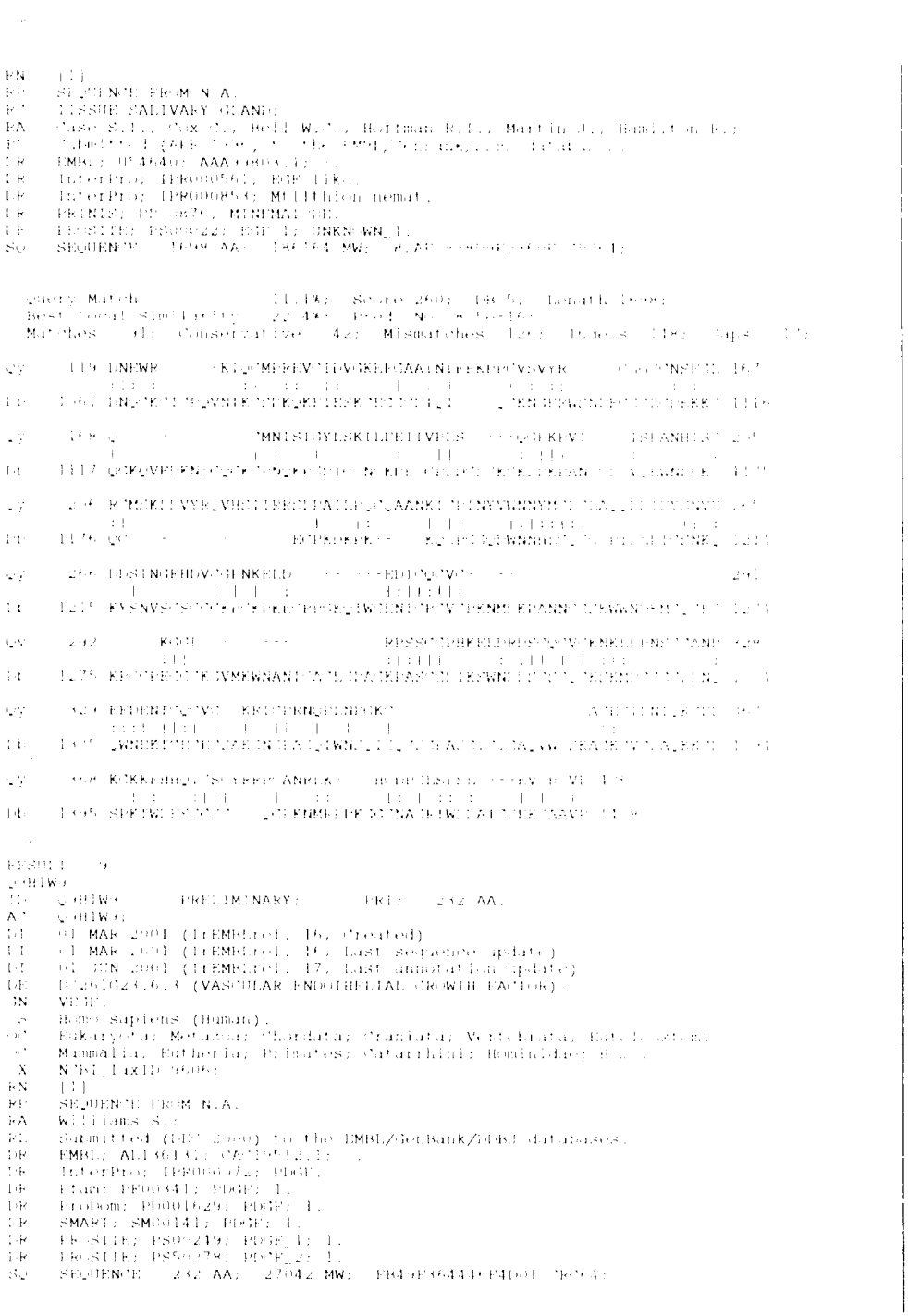
Qy 125 QQCMNESIQYLSKIIEEIVPESQQPKEPVI ISFANEISCPCMSKEIVYRQV 212
Db 1079 INCPARQIIESSESCCPSI PEPCIDVIEPESNEECQVCPEKKCQSKQIIEKNICPE 1134

Qy 213 HSIIRRSLPAIIPQCQAAN KICPFNYVWNNYMCPCL 255
Db 1135 PGGQKWNCNQCQCPCIPAPFCASQKYSCNVICSSCNPCHFAKSCIPSNQVWCENKCQCV 1194

Qy 256 AQQQFEEYSNYVDDSINGFHHAVSFNKLIDGIS QVKKLSESSQFGHKEILGKLSCQE 313
Db 1195 PEE NMESIACN CS NKWWNEKACECPCPEPIEACPKSVQKWNKNICACV 1249

Qy 314 VCKNEFFKQCANKLKHCIDQLSESSEVCKCV 405
Db 1250 ASQQWCSQQCQE SSAISKCFSQAQIWCAKQCKCV 1304

RESULT 2
Q94408
ID Q94408 PRELIMINARY; PRT; 1608 AA.
AC Q94408;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 185 KDA STICK PROTEIN.
GN SF185.
OS Chironomus pallidivittatus (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tra... ...a; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomoidea; Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7151;



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Db    173 QKEKEKKSRYKSWSVYVGARC                                   188

Qy    292 KGGI RPSSCPHKE        IDRISCQCVCKNKLFPNSCGANR FEENIC C 337
             |  |  |||  |         |  :|:| |||     : | |  :    :| |  :
Db    197 PWSLPGPHPCGPCSERRKHLFVQDPQTCKCSCKNT  DSRCKARQLELNERTCRC 219


RESULT  11
Q9MYV3
ID   Q9MYV3       PRELIMINARY;       PRT;   214 AA.
AC   Q9MYV3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 188 PRECURSOR.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20125516; PubMed=10661874;
RA   Scheidegger P., Weiglhofer W., Suarez S., Kaser-Hotz B., Steiner R.,
RA   Ballmer-Hofer K., Jaussi R.;
RT   "Vascular endothelial growth factor (VEGF) and its receptors in tumor-
RT   bearing dogs.";
RL   Biol. Chem. 380:1449-1454(1999).
DR   EMBL; AJ133758; CAB82426.1; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    214       VASCULAR ENDOTHELIAL GROWTH FACTOR 188.
SQ   SEQUENCE   214 AA;  25175 MW;  0AC960A158C44B27 CRC64;

  Query Match             9.5%;  Score 222.5;  DB 6;  Length 214;
  Best Local Similarity   25.5%;  Pred. No. 2.8e-13;
  Matches   64;  Conservative   26;  Mismatches   64;  Indels   97;  Gaps    9;

Qy    109 HYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQ 168
             |   |::| :|  :::: | | |  :|: :|:        ||| || : ||||||| |:|:
Db     34 HKPHEVVKFMD VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLE 92

Qy    169 CMNISTGYLSKTLFEITVPL       SQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIR 222
             |: |            | ||: :        ||       :||  |: | |  | |  ,|      |
Db     93 CVPTEE         FNITMQIMRIKPHQGQHIGEMSFLQHSKCECRPKKDRARQEKKSVRG 145

Qy    223                   RSLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTN 276
                            |   | ::|
Db    146 KGKGQKRKRKKSRYKPWSVP                                             165

Qy    277 GFHDVCGPNKELDEDTCQCVCKGGLRPSSCPHKEL    DRDSCQCVCKNKLFPNSCGAN 327
                ||| ,                                | |    |  :::|  :::        :
Db    166       CGPCSE                           RRKHLFVQDPQTCKCSCKNT  DSRCKAR 198

Qy    328 R FEENTCQC 337
             : | :| ||:|
Db    199 QLELNERTCRC 209


RESULT  12
Q9XSF4
ID   Q9XSF4       PRELIMINARY;       PRT;   208 AA.
AC   Q9XSF4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 182.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Jingjing L., Roque R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133249; AAD29683.1; -.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   208 AA;  24400 MW;  CE77AC39IF5C2BBE CRC64;

  Query Match             9.5%;  Score 221.5;  DB 6;  Length 208;
  Best Local Similarity   26.5%;  Pred. No. 3.4e-13;
  Matches   63;  Conservative   27;  Mismatches   71;  Indels   77;  Gaps    9;

Qy    109 HYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQ 168
             |   |::| :|  :::: | | |  :|: :|:        ||| || : ||||||| |||:
Db     34 HKPHEVVKFMD VYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLE 92

Qy    169 CMNISTGYLSKTLFEITVPL       SQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRR 223
             |: |            | ||: :        ||       :||  |: | |  | |  ||      :|
Db     93 CVPTEE-      -FNITMQIMRIKPHQGQHIGEMSFLQHSKCECRPKKDRARQEKKSVRG 145

Qy    224 SLPATLPQCQAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVCGPNKELD 283
                   | :    |: |                                    ||    |
Db    146 KGKG    QKRKRKKSRP                                    CGPCSE     165

Qy    284 EDTCQCVCKGGLRPSSCPHKEL    DRDSCQCVCKNKLFPNSCGANREFDENTCQC 337
                                  | |    |  :|:| |||     : | |  : | :: ||:|
Db    166                         RRKHLFVQDPQTCKCSCKNT  DSRCKARQLELNERTCRC 203


RESULT  13
O60720
ID   O60720       PRELIMINARY;       PRT;   209 AA.
AC   O60720;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VEGF183 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH FACTOR 183)
DE   (DJ261G23.6.6) (VASCULAR ENDOTHELIAL GROWTH FACTOR).
GN   VEGF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=99096474; PubMed=9878851;
RA   Lei J., Jiang A., Pei D.;
RT   "Identification and characterization of a new splicing variant of
RT   vascular endothelial growth factor: VEGF183.";
RL   Biochim. Biophys. Acta, Gene Struct. Expr. 1443:400-406(1998).
RN   [2]
RP   SEQUENCE OF 114-209 FROM N.A.
RC   TISSUE=RETINA;
RA   Jingjing L., Roque R.S.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Williams S.;
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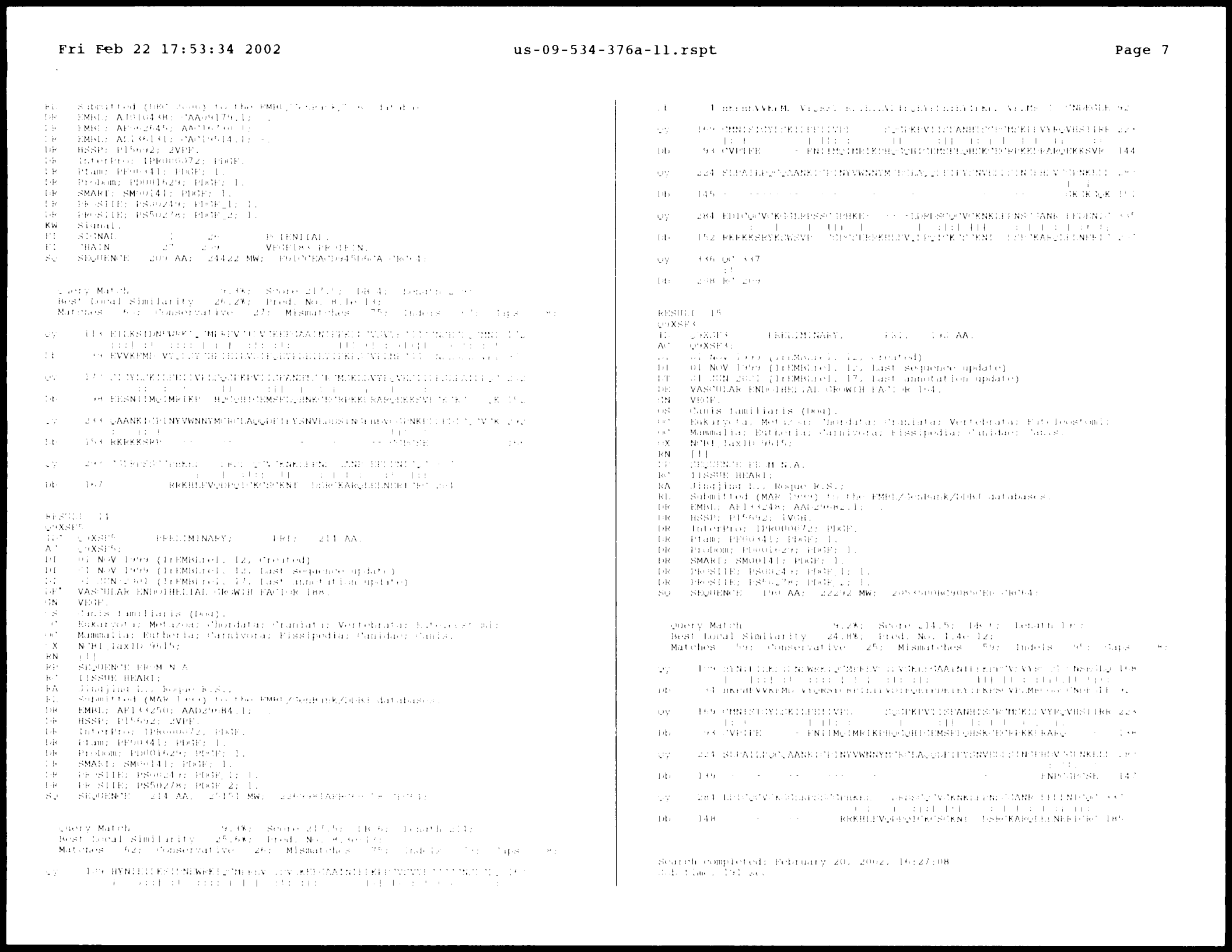

Migration protein search, using sw model

Run on: February 20, 2002, 16:24:42 ; Search time 2.5 Seconds
(without alignments)
801.395 Million cell updates/sec

Title: US-09-534-376A-11
Perfect score: 2855
Sequence: 1 MHLLGFLSLACSLLAAALIP.....SESEEVCKCVLSYWKKPHCN 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100050 seqs, 36604827 residues

Total number of hits satisfying chosen parameters: 200100

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2855	100.0	415	1	VEGC_MOUSE	P49769 Mus musculus
2	2018	87.8	419	1	VEGC_HUMAN	P49767 Homo sapien
3	271.5	11.6	1760	1	BAB3_CHITE	Q99... Chironomus
4	213.5	9.2	215	1	VEGF_HUMAN	P15... Homo sapien
5	213.5	9.1	190	1	VEGF_PIG	P19... Sus scrofa
6	211.5	8.6	190	1	VEGF_RAT	P... Rattus norv
7	198.5	8.5	190	1	VEGF_BOVIN	P... Bos taurus
8	196.5	8.4	164	1	VEGF_CAVPO	P... Cavia porc
9	196.5	8.4	214	1	VEGF_MOUSE	Q... Mus musculus
10	190.5	8.2	473	1	EP2_MYTGA	Q... Mytilus gal
11	174.5	7.7	188	1	VEGB_MOUSE	P... Mus musc...
12	174.5	7.7	188	1	VEGB_HUMAN	P... Homo sapien
13	173.5	7.4	145	1	VEGF_SHEEP	P... Ovis aries
14	173	7.4	216	1	VEGF_CHICK	P... Gallus gal
15	168	7.3	2703	1	NOTC_DROME	P... Drosophila
16	165.5	7.3	133	1	VEGB_OPEN2	P... Ateles (
17	161.5	6.9	1964	1	NTC4_MOUSE	P... Mus musculus
18	160	6.9	148	1	VEGB_OPEN7	P... Ateles (
19	159.5	6.8	3655	1	LMA5_MOUSE	P... Mus musculus
20	155.5	6.7	2482	1	VWF_PIG	P... Sus scrofa
21	155	6.7	2444	1	NTC1_HUMAN	P... Homo sapien
22	152.5	6.6	170	1	PLGF_HUMAN	P... Homo sapien
23	151.5	6.5	2437	1	NOTC_BRARE	P... Brachydan
24	151.5	6.5	2871	1	FBN1_HUMAN	P... Homo sapien
25	151	6.5	3072	1	LML2_CAEEL	Q... Caenorhabdi
26	149	6.4	1552	1	LML1_CAEEL	P... Caenorhabdi
27	148	6.3	2139	1	CRB_DROME	P... Drosophila
28	148	6.3	2813	1	VWF_CANFA	P... Canis fami
29	147.5	6.3	2524	1	NOTC_XENLA	P... Xenopus la
30	147.5	6.3	2531	1	NTC1_MOUSE	P... Mus musculu
31	147.5	6.3	2871	1	FBN1_BOVIN	P... Bos taurus
32	147	6.3	2871	1	FBN1_PIG	P... Sus scrofa
33	146.5	6.3	1790	1	LMB1_DROME	P... Drosophila
34	146	6.3	2871	1	FBN1_MOUSE	P... Mus musc...
35	145.5	6.2	798	1	21B1_XENLA	P... Xenopus lae
36	145.5	6.2	1429	1	LIN2_CAEEL	P... Caenorhabdi
37	145.5	6.2	2907	1	FBN2_MOUSE	P... Mus musculus
38	145.5	6.2	2911	1	FBN2_HUMAN	P... Homo sapien
39	145	6.2	1680	1	EGR2_DROME	P... Drosophila
40	144.5	6.2	1064	1	PAP1_STRPU	P... Strongylocen
41	144	6.2	798	1	21B2_HUMAN	P... Homo sapien
42	142.5	6.1	1746	1	JENA_PIG	Q... Sus scrofa
43	142.5	6.1	2581	1	NTC1_RAT	Q... Rattus norv
44	141	6.0	1808	1	JENA_CHICK	P... Gallus gal
45	141	6.0	2813	1	VWF_HUMAN	P... Homo sapien

ALIGNMENTS

RESULT 1
VEGC_MOUSE
ID VEGC_MOUSE STANDARD; PRT; 415 AA.
AC P97953;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND)
DE (FLT4-L).
GN VEGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=97164597; PubMed=9012504;
RA Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA Joukov V., Alitalo K.;
RT "VEGF-C receptor binding and pattern of expression with VEGFR-3
RT suggests a role in lymphatic vascular development.";
RL Development 122:3829-3837(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=97388462; PubMed=9247156;
RA Pitz I.J., Morris J.C., Fowler E., Ioud A., Burgess P., Greco R.,
RA Wand J., Gassaway R., Nicolaou P., Kocsacio S., Charlotta A.,
RA Giannotti J., Finnerty H., Zollner R., Beier D.R., Look L.V.,
RA Turner K.J., Wood C.R.;
RT "Characterization of murine FLT4 ligand/VEGF-C.";
RL Oncogene 15:618-618(1997).
CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC CELL GROWTH,
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the platelet-derived growth factor
CC family.
CC ---------- ---------- ---------- ----------
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CC ---------- ---------- ---------- ----------
DR EMBL; U73620; AAC52984.1; -.
DR EMBL; U58112; AAB16707.1; -.
DR HSSP; P15692; 1VPF.
DR MGD; MGI:109124; Vegfc.
DR InterPro; IPR002483; PDGF.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; PDGFSUPER.
DR ProDom; PD000220; PDGF; 1.
DR SMART; SM00141; PDGF; 1.

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DR   PROSITE; PS00239; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL          1      ?        POTENTIAL.
FT   PROPEP          ?     108       POTENTIAL.
FT   CHAIN           ?     417       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN        271     961       4 X 24 AA TANDEM REPEATS.
FT   REPEAT        271     294       1.
FT   REPEAT        295     318       2.
FT   REPEAT        319     342       3.
FT   REPEAT        343     361       4 (PARTIAL).
FT   CARBOHYD      171     171       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      203     203       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      296     296       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   417 AA;  46471 MW;  DDDSDDDDCLCCCSSDDD CRC64;


  Query Match             100.0%;  Score 2333;  DB 1;  Length 417;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-172;
  Matches  417;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MHLLGFSLACSLLAAALLPGPREAPAIVAAELEVGLGESEAELTRSRKRAIVAAFEEGGDPGELVLALSTRDVHL 90
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Db       1 MHLLGFSLACSLLAAALLPGPREAPAIVAAELEVGLGESEAELTRSRKRAIVAAFEEGGDPGELVLALSTRDVHL 90

Qy      91 RSVQQPSTSDSNILVERAERGSWANMEKTQPKSWSGPLSSKKLNPLVRIHSVKTAAARSSYLEMEVSYVTKMYK 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 RSVQQVELEMEVEYPFAWKMYKTQPRCQWSGPLSSKKLNPLVRIHSVKTAAARSSYLEMEVSYVTKMYK 160

Qy     161 EWEKEQPMPRELVTLVSKELPDAAINEFEKRFQTVSVYMKQGQYDNPSSGPVMNLSLDYEDKT 224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 EWEKEQPMPRELVTLVSKELPDAAINEFEKRFQTVSVYMKQGQYDNPSSGPVMNLSLDYEDKT 224

Qy     225 LFELTVFGLSQKPERGLFSGTIDVFYRQVRCSIPRSLEFAIFQPSAANKETP 277
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     225 LFELTVFGLSQKPERGLFSGTIDVFYRQVRCSIPRSLEFAIFQPSAANKETP 277

Qy     278 INYVWNNYMPKPLAQDFTPYSNVEHGRSINGFHDVCGPNKELDEDCQVTCKTGLPS 334
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Db     278 INYVWNNYMPKPLAQDFTPYSNVEHGRSINGFHDVCGPNKELDEDCQVTCKTGLPS 334

Qy     335 GPHKELDRDSKQAQVVKNKLPPNSKSANREIHENPQPVKKSTPENLLNPCAASPHR 391
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Db     335 GPHKELDRDSKQAQVVKNKLPPNSKSANREIHENPQPVKKSTPENLLNPCAASPHR 391

Qy     392 NTQKQFELKGKEHHQPSSYPRPPANKLKHCDPSLESGEEVCPCVPSYWKEPHENH 445
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RESULT  2
VEGC_HUMAN
ID   VEGC_HUMAN     STANDARD;      PRT;   419 AA.
AC   P49767;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
DE   ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4
DE   L).
GN   VEGFC.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX   MEDLINE=96176121; PubMed=8617204;
RA   Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA   Saksela O., Kalkkinen N., Alitalo K.;
RT   "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT   the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL   EMBO J. 15:290-298(1996).
RN   [2]
RP   ERRATUM.
RX   MEDLINE=96203094; PubMed=8617200;
RA   Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA   Saksela O., Kalkkinen N., Alitalo K.;
RL   EMBO J. 15:1751-1751(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96412526; PubMed=8700872;
RA   Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RT   "Vascular endothelial growth factor-related protein: a ligand and
RT   specific activator of the tyrosine kinase receptor Flt4.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Fitzpatrick L., Morris D.C., Bowler P.S., Jones A.L., Greene F.,
RA   Petrova P., Ciannotti J., Ciarletta A., Bennessey D., Kozarich J.,
RA   Fitzgerald M., Scaltreto H., Welch N., Nelson S., Finnerty H.,
RA   Zollner R., Wand J., Nicklaus E., Gasiewicz R., Turner K.,
RA   Wood C.R.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC   -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, PLACENTA,
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X94216; CAA64007.1; -.
DR   EMBL; U43142; AAA85214.1; -.
DR   EMBL; U73711; AAB52009.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601528; -.
DR   InterPro; IPR00400; GF_cysknot.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00749; GFCYSTKNOT.
DR   Prodom; Prodom629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL          1      ?        POTENTIAL.
FT   PROPEP          ?     102       POTENTIAL.
FT   CHAIN         103     419       VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN        275     965       4 X 24 AA TANDEM REPEATS.
FT   REPEAT        275     298       1.
FT   REPEAT        299     322       2.
FT   REPEAT        323     346       3.
FT   REPEAT        347     365       4 (PARTIAL).
FT   CARBOHYD      175     175       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      207     207       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      240     240       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   419 AA;  46903 MW;  9E508716D9E61AFC CRC64;


  Query Match             87.8%;  Score 2048;  DB 1;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 4.2e-156;
  Matches  358;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFSLACSLLAAALLPGPREAPAIVAAELEVGLGESEAELTRSRKRAIVAAFEEGGDPGELVLALSTRDVHL 90
           |||| | |||||||||||| ||||||  |||||||  |||||| ||||| || ||  |||| ||
Db       1 MHLSRFSWVASLLAAALIPPSREAPAAAAAELEVGLNAREAGVRAIAYASKQIELAG 57

Qy      91 RSVQQPSTSDSNILVERAERGSWANMEKTQPKSWSGPLSSKKLNPLVRIHSVKTAAARSSYLEMEVSYVTKMYK 160
           |||||||||||||||||||||||||||||||||    ||||||  |||||||||||||||||||||||||||||
Db      58 RSVQEVELEMEVEYPFAWKMYKTQPRCQWS----PLSSKKLNPLVRIHSVKTAAARSSYLEMEVSYVTKMYK 123

Qy     161 EWEKEQPMPRELVTLVSKELPDAAINEFEKRFQTVSVYMKQGQYDNPSSGPVMNLSLDYEDKT 224
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 EWEKEQPMPRELVTLVSKELPDAAINEFEKRFQTVSVYMKQGQYDNPSSGPVMNLSLDYEDKT 187

Qy     225 LFELTVFGLSQKPERGLFSGTIDVFYRQVRCSIPRSLEFAIFQPSAANKETP 277
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 LFELTVFGLSQKPERGLFSGTIDVFYRQVRCSIPRSLEFAIFQPSAANKETP 240

Qy     278 INYVWNNYMPKPLAQDFTPYSNVEHGRSINGFHDVCGPNKELDEDCQVTCKTGLPS 334
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 INYVWNNYMPKPLAQDFTPYSNVEHGRSINGFHDVCGPNKELDEDCQVTCKTGLPS 297

Qy     335 GPHKELDRDSKQAQVVKNKLPPNSKSANREIHENPQPVKKSTPENLLNPCAASPHR 391
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 GPHKELDRDSKQAQVVKNKLPPNSKSANREIHENPQPVKKSTPENLLNPCAASPHR 354

Qy     392 NTQKQFELKGKEHHQPSSYPRPPANKLKHCDPSLESGEEVCPCVPSYWKEPHENH 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 NTQKQFELKGKEHHQPSSYPRPPANKLKHCDPSLESGEEVCPCVPSYWKEPHENH 408
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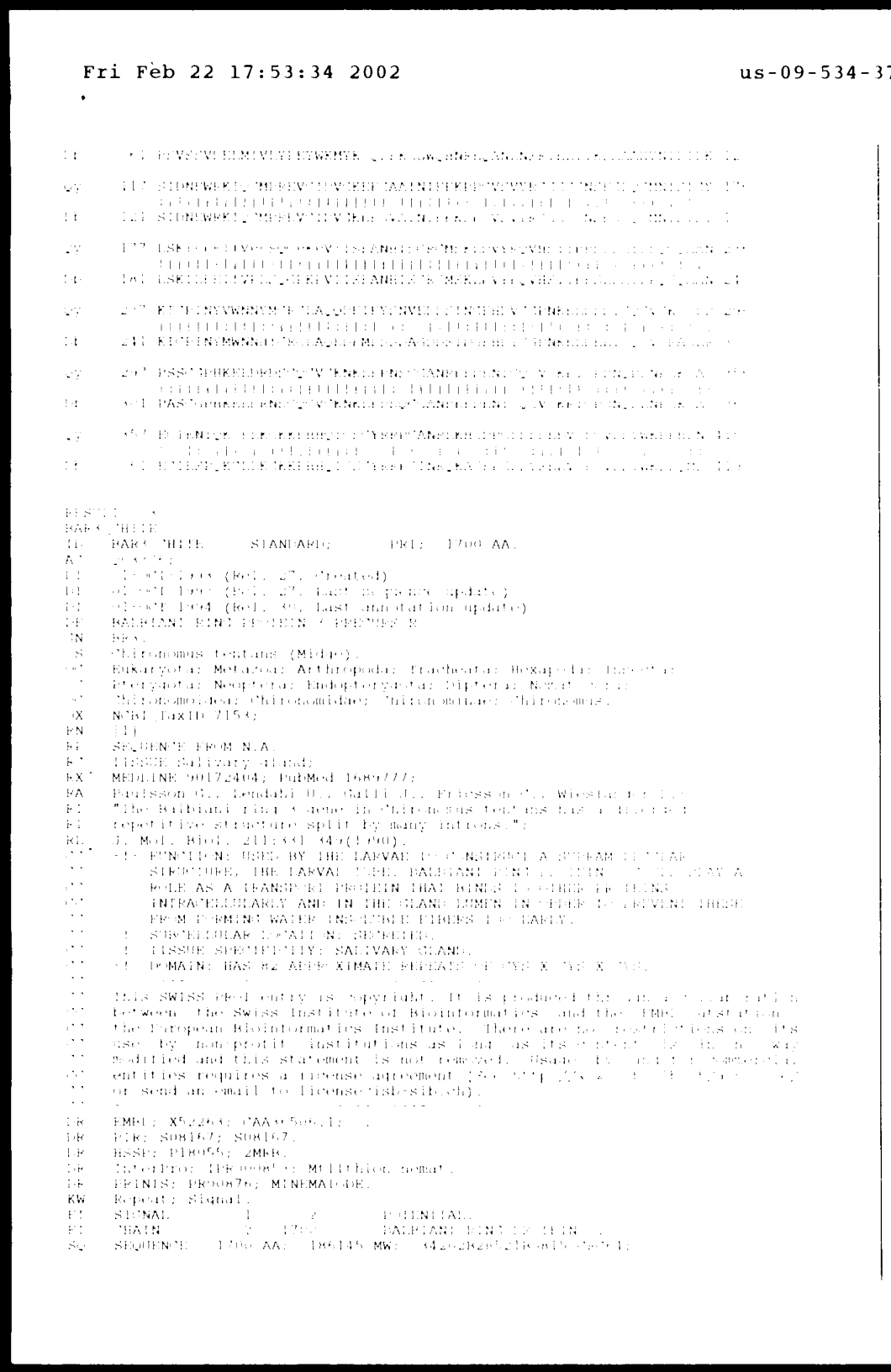

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RL   J. Biol. Chem. 266:11947-11954(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 92218700; PubMed 1567095;
RA   Weindel K., Marme D., Weich H.A.;
RT   "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT   endothelial growth factor.";
RL   Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN   [5]
RP   PRELIMINARY SEQUENCE OF 27-46; 43-50 AND 59-81.
RX   MEDLINE 90062112; PubMed 2584205;
RA   Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA   Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT   "Human vascular permeability factor. Isolation from U937 cells.";
RL   J. Biol. Chem. 264:20017-20024(1989).
RN   [6]
RP   SEQUENCE OF 27-41.
RX   MEDLINE 93145946; PubMed 7678805;
RA   Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
RA   Kochs G., Marme D., Hug H., Weich H.A.;
RT   "Synthesis and assembly of functionally active human vascular
RT   endothelial growth factor homodimers in insect cells.";
RL   Eur. J. Biochem. 211:19-26(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX   MEDLINE 97352774; PubMed 9207067;
RA   Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA   de Vos A.M.;
RT   "Vascular endothelial growth factor: crystal structure and functional
RT   mapping of the kinase domain receptor binding site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX   MEDLINE 98035455; PubMed 9351807;
RA   Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT   "The crystal structure of vascular endothelial growth factor (VEGF)
RT   refined to 1.93 A resolution: multiple copy flexibility and receptor
RT   binding.";
RL   Structure 5:1325-1338(1997).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX   MEDLINE 99119204; PubMed 9922142;
RA   Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA   Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT   "Crystal structure of the complex between VEGF and a receptor-blocking
RT   peptide.";
RL   Biochemistry 37:17765-17772(1998).
RN   [10]
RP   STRUCTURE BY NMR OF 34-135.
RX   MEDLINE 97477919; PubMed 9336848;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "1H, 13C, and 15N backbone assignment and secondary structure of the
RT   receptor-binding domain of vascular endothelial growth factor.";
RL   Protein Sci. 6:2250-2260(1997).
RN   [11]
RP   STRUCTURE BY NMR OF 137-215.
RX   MEDLINE 98208410; PubMed 9634701;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "Solution structure of the heparin-binding domain of vascular
RT   endothelial growth factor.";
RL   Structure 6:637-648(1998).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE (VEGF 121, VEGF 165,
CC       VEGF 189 AND VEGF 215).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M32977; AAA35789.1; -.
DR   EMBL; M27281; AAA36807.1; -.
DR   EMBL; M63978; AAA36804.1; -.
DR   EMBL; M63971; AAA36804.1; JOINED.
DR   EMBL; M63972; AAA36804.1; JOINED.
DR   EMBL; M63973; AAA36804.1; JOINED.
DR   EMBL; M63974; AAA36804.1; JOINED.
DR   EMBL; M63975; AAA36804.1; JOINED.
DR   EMBL; M63976; AAA36804.1; JOINED.
DR   EMBL; M63977; AAA36804.1; JOINED.
DR   EMBL; X62568; CAA44447.1; -.
DR   PIR; A34492; A34492.
DR   PIR; A40079; A40079.
DR   PIR; A40080; A40080.
DR   PIR; A40454; A40454.
DR   PIR; B40454; B40454.
DR   PIR; C40454; C40454.
DR   PIR; JQ1463; JQ1463.
DR   PIR; JQ1464; JQ1464.
DR   PIR; S17348; S17348.
DR   PDB; 1VGH; 08-APR-98.
DR   PDB; 2VGH; 08-APR-98.
DR   PDB; 1VPF; 08-APR-98.
DR   PDB; 2VPF; 29-JUL-98.
DR   PDB; 1VPP; 23-FEB-99.
DR   MIM; 192240; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal;
KW   3D-structure.
FT   SIGNAL        1     26
FT   CHAIN        27    215       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     52     94
FT   DISULFID     83    128
FT   DISULFID     87    130
FT   DISULFID     77     77       INTERCHAIN.
FT   DISULFID     86     86       INTERCHAIN.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC...).
FT   VARSPLIC    141    141       K -> N (IN ISOFORM VEGF 121 AND ISOFORM
FT                                VEGF 165).
FT   VARSPLIC    142    165       MISSING (IN ISOFORM VEGF 165).
FT   VARSPLIC    142    209       MISSING (IN ISOFORM VEGF 121).
SQ   SEQUENCE   215 AA;  25173 MW;  7B0759AB5871FE33 CRC64;

  Query Match              9.2%;  Score 213.5;  DB 1;  Length 215;
  Best Local Similarity    25.3%;  Pred. No. 3.5e-16;
  Matches   59;  Conservative   26;  Mismatches   79;  Indels   69;  Gaps    5;

Qy        [illegible] NEWRKTQ MRPEV [illegible] AAINLEEE [illegible] NS [illegible] MNL 172
              [illegible]
Db         39 EVVKFMD VYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 97

Qy        [illegible] ANRLSTRNSKLDVYRQVHSIIRRSLPATLPQC 232
              [illegible]
Db         98 EESNITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVR          145

Qy        233 QAANKTCPTNYVWNNYMCRCLAQQDFIFYSNVEDDSTNGFHDVCGPNKELDEDTCQCVCK 292
              [illegible]
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Db    116                                                  GKGKKQ_RPRERKRSPYK 141

Qy    293 GSLPRLS*TDHEE  **  *LPW*S*S*VSAWL*ENR*SANS EILSN 327
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Db    142 SWSVP  GGP*SERKKHLRVQDP*I*R*CSCSNI  DSP*KARQLELNERIC*K* 200


RESULT  5
VEGF_PIG
ID   VEGF_PIG        STANDARD;       PRT;   232 AA.
AC   P49151;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=95143284; PubMed=7841283;
RA   Sharma H.S., Tana Z.H., Gho B.C.H., Verbouw P.D.;
RT   "Nucleotide sequence and expression of the porcine vascular
RT   endothelial growth factor.";
RL   Biochim. Biophys. Acta 1260:235-238(1995).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC       CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; X64363; CAA45743.1; -.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   190 AA;  22299 MW;  0A01C0B0279A3F3F CRC64;


  Query Match             9.1%;  Score 211.5;  DB 1;  Length 190;
  Best Local Similarity   24.8%;  Pred. No. 4.2e-10;
  Matches   58;  Conservative   24;  Mismatches   57;  Indels    4;  Gaps    8;

Qy    113 EIEFSQIQNEWREKQCMPRECVELVVDVGSEFGAINTTIKPSCVSVYRCNGVCGDNN 172
          |:|:|:|  :::: | | :  :|: :|:     ||| || : |||||||:|:::|
Db     38 EVVKEMD VYQRSVCRGLETLVDISQSYVHCQPLDDYPLEVDEYHSQIQEVER 90


Qy    173 SIGYLSFLLPDVTISFANDTGCVMKSRDVEVWGIVSILTGRSLFA 217
                  | ||: :      ||     :|| | | | | | ||
Db     97 EE-------FNLIMQTMKLEFRGQGLGTCEMSSFLGNEVEFRTRAKQ    138

Qy    218 TLPQKLAANEICLNIYVWNNYMCVAGSFLEYSSNVPLGFSNCSRGVVGSRFFLDEDTC 277
                                                    : ||| |
Db    139 -  -  --  --  --  --  --  --  --  --  --  ENDCGPCSE    147

Qy    278 QCVTRCGLRKFEDCCVEQT  TRLSV_VTPNELFNLTTANGNSTTPNTYC 327
                  ||   |  :|:| |||    : | | : | :|| |||
Db    148 -------  ------RRKHLEVQLPLPSDKVNMSFCHNKSAKIKCNFTCKT 185


RESULT  6
VEGF_RAT
ID   VEGF_RAT        STANDARD;       PRT;   190 AA.
AC   P16612;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-190.
RX   MEDLINE=90297240; PubMed=2320579;
RA   Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
RA   Palisi T.M., Hope D.A., Thomas K.A.;
RT   "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT   that is homologous to platelet-derived growth factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2628-2632(1990).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC       CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY GLAND, IN
CC       PARTICULARLY IN SUPRAOPTIC AND PARAVENTRICULAR NUCLEI AND THE
CC       CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF
CC       THE OVARY AND IN KIDNEY GLOMERULI.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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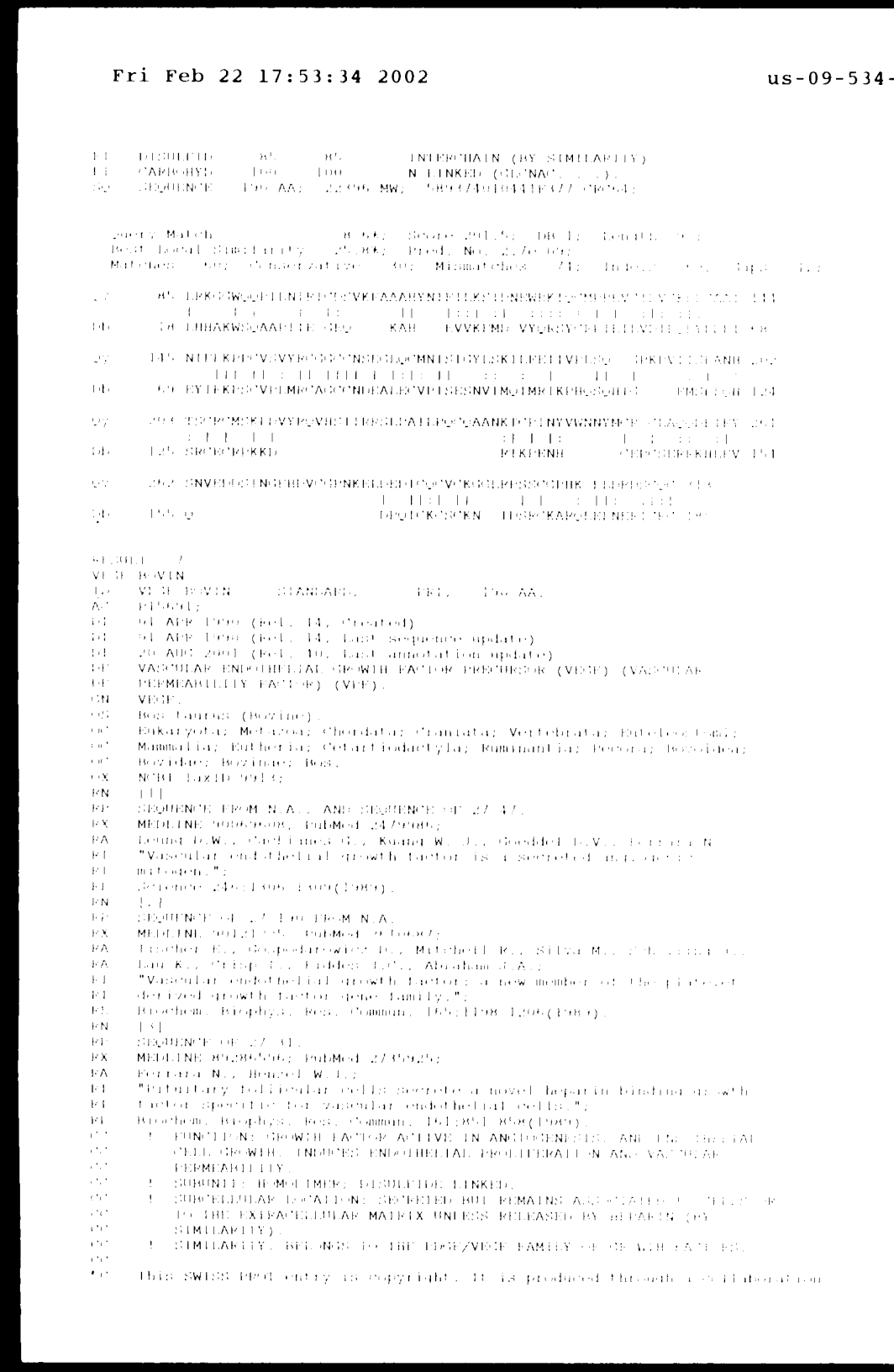
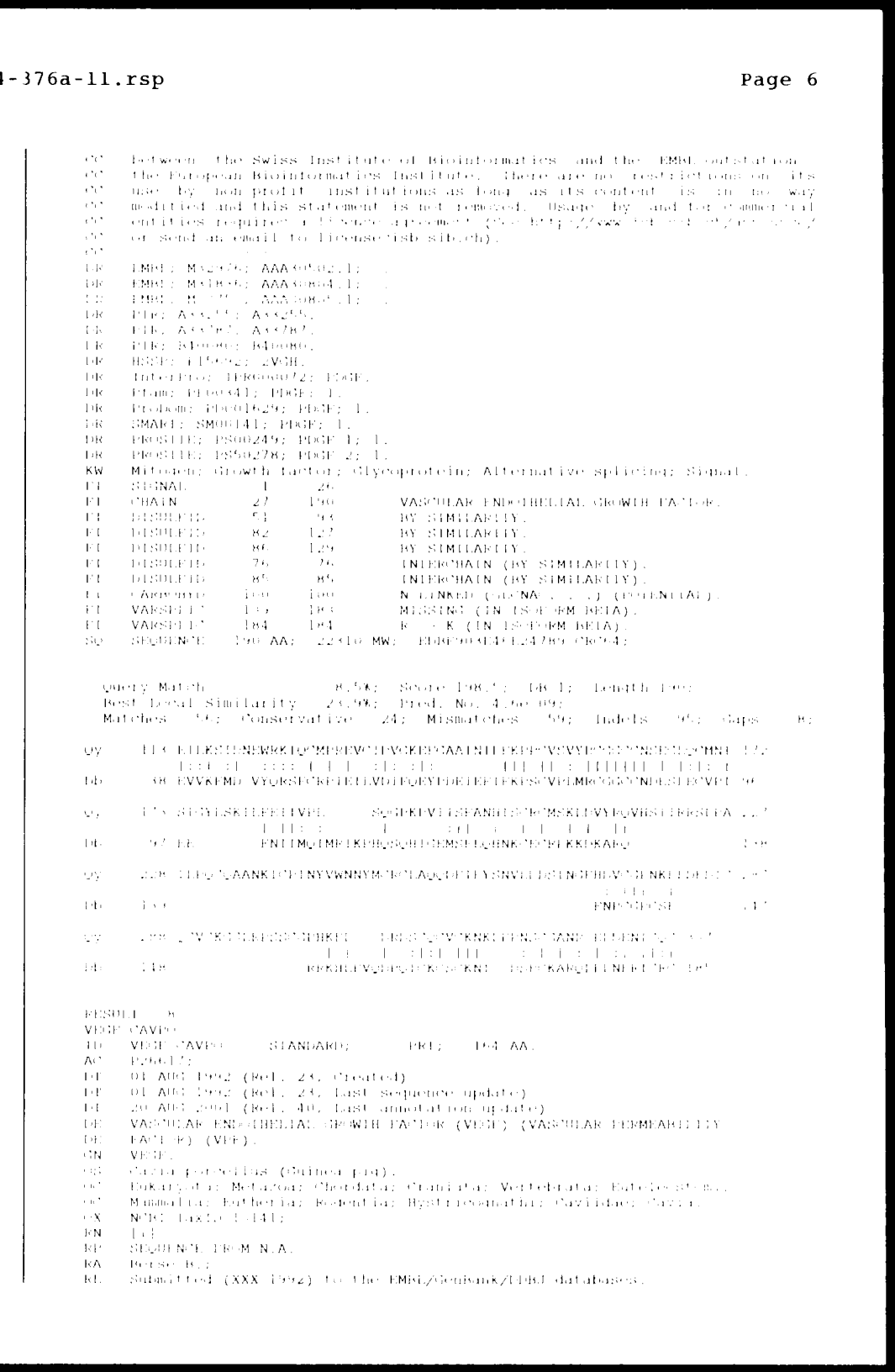
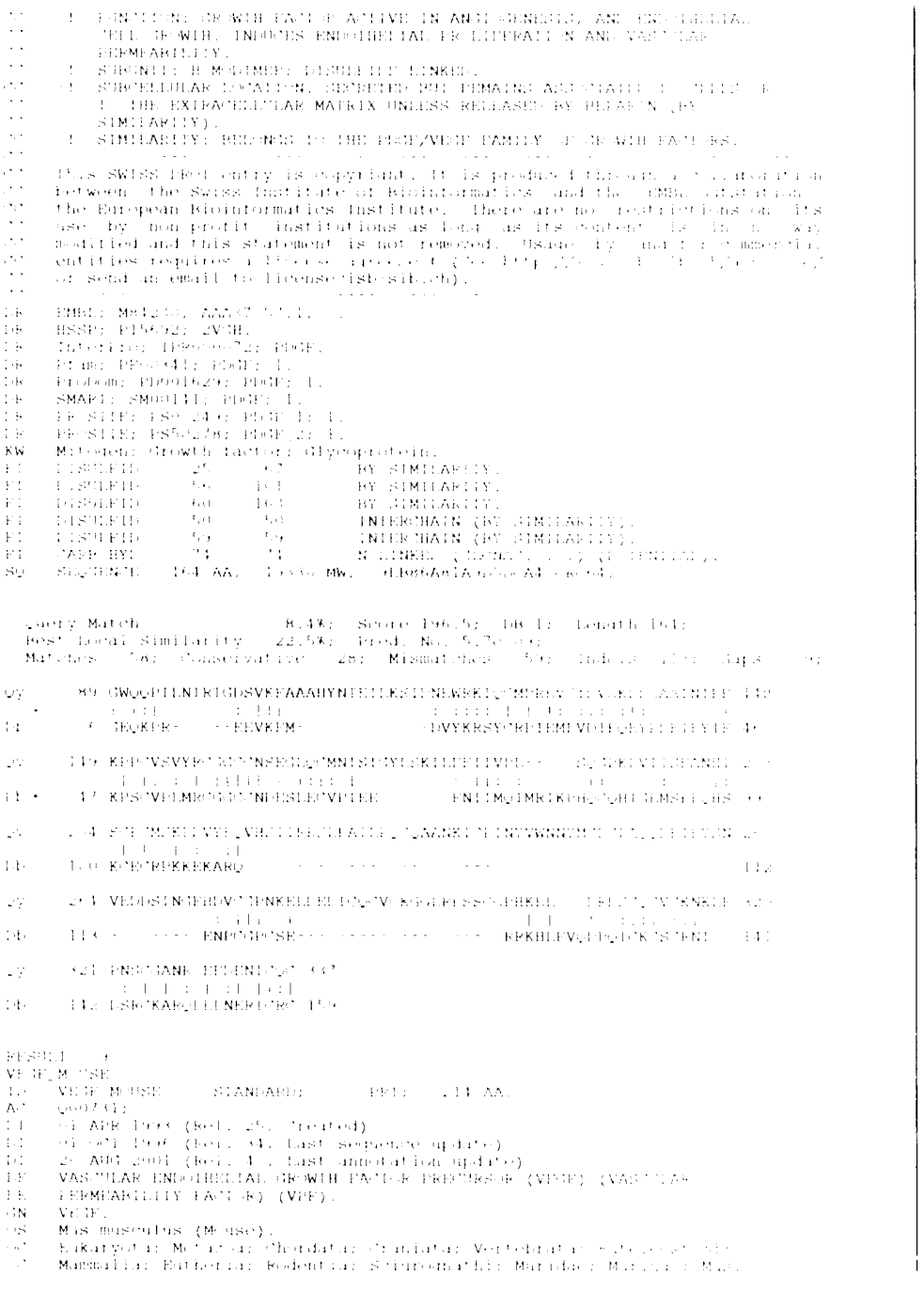
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; M32167; AAA41211.1; -.
DR   PIR; A35987; A35987.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
```






CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC ! SUBUNIT: B HOMODIMER; DISULFIDE LINKED.
CC ! SUBCELLULAR LOCATION: SECRETED PDF REMAINS ASSOCIATED TO CELLS
CC ! THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC ! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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DR EMBL; M63191; AAA37571.1; -.
DR HSSP; P15692; 2VGH.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD000629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 214 VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT DISULFID 61 163 BY SIMILARITY.
FT DISULFID 80 168 INTERCHAIN (BY SIMILARITY).
FT DISULFID 82 170 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 214 AA; 23944 MW; 4BB6DA1A6C6C4A1 CRC64;

Query Match 8.4%; Score 196.5; DB 1; Length 214;
Best Local Similarity 22.5%; Pred. No. 5.7e-09;
Matches 56; Conservative 28; Mismatches 59; Indels 43; Gaps 9;
RESULT 1
VEGF_MOUSE
ID VEGF_MOUSE STANDARD; PRT; 214 AA.
AC Q00731;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-APR-2001 (Rel. 41, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX MEDLINE; 92274865; PubMed=1592368;
RA Breier G., Albrecht U., Sterrer S., Risau W.;
RT "Expression of vascular endothelial growth factor during embryonic
RT angiogenesis and endothelial cell differentiation.";
RL Development 114:521-532(1992).
RN [2]
RP SEQUENCE FROM N.A. (VEGF 1).
RX MEDLINE; 92355595; PubMed=1644816;
RA Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT "Vascular endothelial growth factor. Regulation by cell
RT differentiation and activated second messenger pathways.";
RL J. Biol. Chem. 267:16317-16322(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96216498; PubMed=8663007;
RA Shima D.T., Kuroki M., Deutsch U., Ng Y.S., Adamis A.P., D'Amore P.A.;
RT "The mouse gene for vascular endothelial growth factor. Genomic
RT structure, definition of the transcriptional unit, and
RT characterization of transcriptional and post-transcriptional
RT regulatory sequences.";
RL J. Biol. Chem. 271:3077-3083(1996).
CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC ! SUBUNIT: B HOMODIMER; DISULFIDE LINKED.
CC ! ALTERNATIVE SPLICING: THREE FORMS (VEGF 1, VEGF 2 AND VEGF 3) ARE
CC PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC LONGEST FORM (VEGF 3, SHOWN HERE) CONTAINS A PASC- INSERT LINKED
CC TO CELL ASSOCIATION/HEPARIN BINDING.
CC -!- TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN
CC THE CHOROID PLEXUS, PARAVENTICULAR NEUROEPITHELIUM, PLACENTA AND
CC KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL
CC GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF
CC VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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DR EMBL; S37052; AAB22052.1; -.
DR EMBL; S37053; AAB22053.1; -.
DR EMBL; S38100; AAB22054.1; -.
DR EMBL; M95200; AAA40547.1; -.
DR EMBL; D41383; -; NOT_ANNOTATED_CDS.
DR PIR; A41851; A41851.
DR HSSP; P15692; 2VGH.
DR MIM; 601704; VEGF.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD000629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 214 VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT DISULFID 61 163 BY SIMILARITY.
FT DISULFID 82 167 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).

```
FT   VARSPLIC*     130     180        K    N (IN ISOFORM VIGF 1).
FT   VARSPLIC*     131     164        MISSING (IN ISOFORM VIGF 3).
FT   VARSPLIC*     131     208        MISSING (IN ISOFORM VIGF 2).
FT   CONFLICT      117     118        GE   ER (IN REF. 2).
SQ   SEQUENCE   211 AA;  25283 MW;  8A7543A5E143B0CE17 CRC64;


  Query Match             8.1%;  Score 196.5;  DB 1;  Length 211;
  Best Local Similarity   25.5%;  Pred. No. 9e-09;
  Matches   52;  Conservative   34;  Mismatches   84;  Indels   21;  Gaps   7;

Qy      113 EILKGIDNEWRKIQKMPFIVKIEVGKEIGAAINIIEKDPK*VEVWK*GI*NEKCGQMMN 172
            |:|:|: |:|:| | | | |:| :|:        ||| || : |: |:|:* |:|:| *
Db       98 EVIKPME*VV*ESV*PFIEIEVKEIPGIEYPGCIEVIEKDP*VEIME*A*I*NLAIE*VI 39

Qy      173 GI*YLGKILFKEIVPLSQ* *PKEPVIISFANHLS*G*MSKIEVYP*VRCIIR*IIAIA 229
            |  :: :  |   II  |     :|| |: | | |  |  :    :|
Db       97 SEGNIEMQIMFIKPHQEQQIG    EMSFLQHSRGTG*KKKIGKIEKKKGVP*K      1 147

Qy      230 Q*QAANKIG*PINYVWNNYMG*K*LAQQDFIFYSNVEDDSINGEHIDVGGPNKEIDEIG*V 289
            : |  :       |: :  | :: :|                                  :
Db      148 KQQEKKKKKKGKIKGWSVH*EP*SEKKKHIPVQ                          192

Qy      290 *PGGLPFSG*SPHK EIMMDSQ* 314
            ||    | |   : ||  :|:|
Db      193 *KN  IDGP*KAPQLEINEKIG* 209


RESULT  1
MYEGA_
ID   EP2_MYEGA      STANDARD;      PRT;   473 AA.
AC   Q27464;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   20-APR-2001 (Rel. 1, Last annotation update)
DE   ADHESIVE PLAQUE MATRIX PROTEIN 2 PRECURSOR (Foot protein 2) (MGFP-
DE   (MGFP 2).
GN   EP2.
OS   Mytilus galloprovincialis (Mediterranean mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytilidae;
OC   Mytilinae; Mytilus.
OX   NCBI_TaxID=29158;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Foot;
RX   MEDLINE=96204164; PubMed=8626812;
RA   Inoue K., Takeuchi Y., Miki D., Odo S.;
RT   "Mussel adhesive plaque protein gene is a novel member of epidermal
RT   growth factor-like gene family.";
RL   J. Biol. Chem. 270:6608-6701(1995).
CC   -!- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S BYSSAL THREAD
CC       PROBABLY ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S
CC       ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A
CC       FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION STARTS AT THE EARLY STAGE OF
CC       FORMATION, STAGE.
CC   -!- PTM: SOME TYROSINES ARE HYDROXYLATED (THIS PROTEIN IS A
CC       DIHYDROXYPHENYLALANINE).
CC   -!- SIMILARITY: CONTAINS 11 EGF LIKE DOMAINS.
CC
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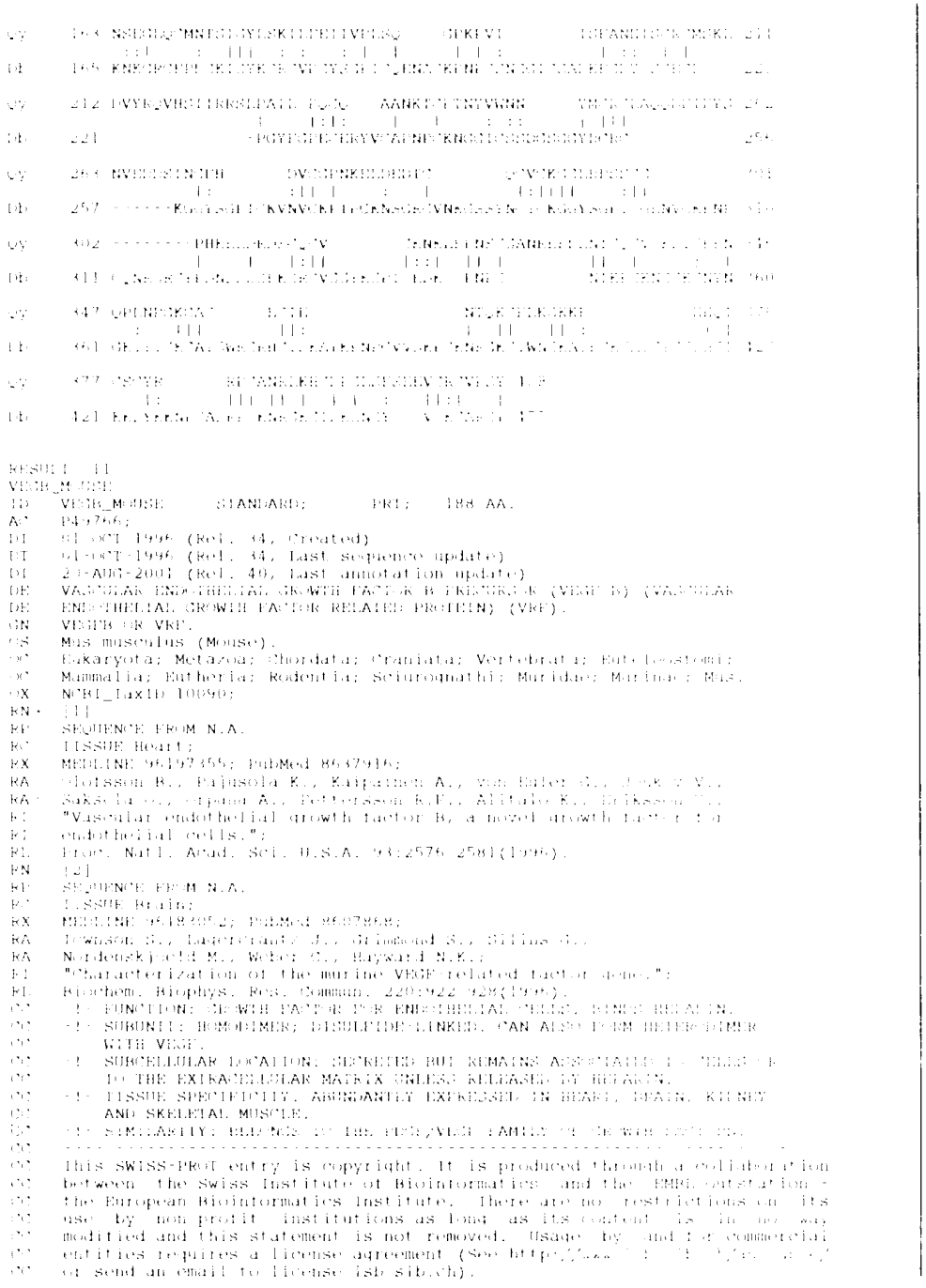
CC
DR   EMBL; D43704; BAA07855.1; -.
DR   InterPro; IPR000152; Asx hydroxyl.
DR   InterPro; IPR000561; EGF like.
DR   InterPro; IPR000742; EGF 2.
DR   InterPro; IPR000803; EGF Ca.
DR   Pfam; PF00008; EGF; 11.
DR   SMART; SM00181; EGF; 10.
DR   PROSITE; PS00010; ASX_HYDROXYL; 2.
DR   PROSITE; PS00022; EGF_1; 11.
DR   PROSITE; PS01186; EGF_2; 10.
KW   Glycoprotein; EGF like domain; Repeat; Signal; Hydroxylation.
FT   SIGNAL        1     17        POTENTIAL.
FT   CHAIN        18    473        ADHESIVE PLAQUE MATRIX PROTEIN 2.
FT   DOMAIN       45     81        EGF LIKE 1.
FT   DOMAIN       83    117        EGF LIKE 2.
FT   DOMAIN      118    154        EGF LIKE 3.
FT   DOMAIN      155    191        EGF LIKE 4.
FT   DOMAIN      192    228        EGF LIKE 5.
FT   DOMAIN      229    265        EGF LIKE 6.
FT   DOMAIN      266    301        EGF LIKE 7.
FT   DOMAIN      302    340        EGF LIKE 8.
FT   DOMAIN      342    378        EGF LIKE 9.
FT   DOMAIN      383    420        EGF LIKE 10.
FT   DOMAIN      425    461        EGF LIKE 11.
FT   MOD_RES      23     23        DOPA.
FT   MOD_RES      31     31        DOPA.
FT   MOD_RES      39     39        DOPA.
FT   MOD_RES      43     43        DOPA.
FT   CARBOHYD     93     93        N-LINKED (GLCNAC...) (POTENTIAL)
FT   DISULFID     46     60        BY SIMILARITY.
FT   DISULFID     54     69        BY SIMILARITY.
FT   DISULFID     71     80        BY SIMILARITY.
FT   DISULFID     86     97        BY SIMILARITY.
FT   DISULFID     91    106        BY SIMILARITY.
FT   DISULFID    108    117        BY SIMILARITY.
FT   DISULFID    122    133        BY SIMILARITY.
FT   DISULFID    127    141        BY SIMILARITY.
FT   DISULFID    145    154        BY SIMILARITY.
FT   DISULFID    159    170        BY SIMILARITY.
FT   DISULFID    174    186        BY SIMILARITY.
FT   DISULFID    182    191        BY SIMILARITY.
FT   DISULFID    196    207        BY SIMILARITY.
FT   DISULFID    201    217        BY SIMILARITY.
FT   DISULFID    219    228        BY SIMILARITY.
FT   DISULFID    233    244        BY SIMILARITY.
FT   DISULFID    238    254        BY SIMILARITY.
FT   DISULFID    256    265        BY SIMILARITY.
FT   DISULFID    270    291        BY SIMILARITY.
FT   DISULFID    275    290        BY SIMILARITY.
FT   DISULFID    292    301        BY SIMILARITY.
FT   DISULFID    306    317        BY SIMILARITY.
FT   DISULFID    311    328        BY SIMILARITY.
FT   DISULFID    330    339        BY SIMILARITY.
FT   DISULFID    346    357        BY SIMILARITY.
FT   DISULFID    351    366        BY SIMILARITY.
FT   DISULFID    368    377        BY SIMILARITY.
FT   DISULFID    387    399        BY SIMILARITY.
FT   DISULFID    393    408        BY SIMILARITY.
FT   DISULFID    410    419        BY SIMILARITY.
FT   DISULFID    429    440        BY SIMILARITY.
FT   DISULFID    434    449        BY SIMILARITY.
FT   DISULFID    451    460        BY SIMILARITY.
SQ   SEQUENCE   473 AA;  51772 MW;  8A70BA8C9BA40A0E CRC64;


  Query Match             8.2%;  Score 196.5;  DB 1;  Length 473;
  Best Local Similarity   21.4%;  Pred. No. 5.1e-08;
  Matches   99;  Conservative   70;  Mismatches  125;  Indels  109;  Gaps   27;

Qy       81 YK*QLEK*GWQQPIENIKIGGGVKEAAAIYNIEILKSTDNEWKKIQ*MEKEVIEVGKEI 140
              :|:   :|||:                  ||      :::|  :  ||  :  :: |||  :
Db       67 YK* P*KGGYY                   GYN*    NEKNA*KPNQ*KNKSD*VIEVGKIE 104

Qy      141 GAA            INIEEKPN*          V*VYK*   GG           *    * E.
                           |  ||               : :||   ||           *    *
Db      105 A*V*PN NEGPIQ PKNV SENP*KNNGK*SPIGNGGKG*KG*GNGKGP*EVHA*KPNP* 164
```



RESULT 11
VEGB_MOUSE
ID VEGB_MOUSE STANDARD; PRT; 188 AA.
AC P49766;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN VEGFB OR VRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96197455; PubMed=8647916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98189052; PubMed=9607868;
RA Townson S., Lagercrantz J., Grimmond S., Silins G.,
RA Nordenskjoeld M., Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene.";
RL Biochem. Biophys. Res. Commun. 229:922-928(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
CC AND SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC ---
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DR EMBL; U48980; AAB94274.1; -.
DR EMBL; U43837; AAC52553.1; -.
DR HSSP; P15692; 2VGH.
DR MGD; MGI:106199; Vegfb.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD000629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Signal; Heparin-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 189 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21442 MW; D52A055FB995E90A CRC64;

Query: match 77.2%; score 279.5; DB 1; length 188;
Best Local Similarity 47.1%; Pred. No. 1.5e-07;
Matches 82; Conservative 43; Mismatches 77; Indels 4; Gaps 2;

RESULT 12
VEGB_HUMAN
ID VEGB_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
DE FACTOR).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96197455; PubMed=8647916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97077124; PubMed=8919691;
RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
RA Pollock P., Gorley P., Cussen L., Ferkir S., Nordenskjoeld M., Ward L.,
RA Hayward N., Weber G.;
RT "Cloning and characterization of a novel human gene related to
RT vascular endothelial growth factor.";
RL Genome Res. 6:124-131(1996).
CC ! FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED. CAN ALSO FORM HETERODIMER
CC WITH VEGF.
CC ! SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR

```
CC       1- THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC    !  TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT CARTILAGE,
CC       HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND LUNG.
CC    !  SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; D48801; AAB06274.1; -.
DR   EMBL; D43636; AAA91163.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601698; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD000629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00240; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Mitogen; Growth factor; Signal; Heparin binding.
FT   SIGNAL          1     21       POTENTIAL.
FT   CHAIN          22    189       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   189 AA;  21291 MW;  FD4D5AD9A472A7D4 CRC64;

  Query Match             7.7%;  Score 178.5;  DB 1;  Length 189;
  Best Local Similarity   27.5%;  Pred. No. 1.6e-07;
  Matches   52;  Conservative   28;  Mismatches   75;  Indels   11;  Gaps    7;

Qy      107 AAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQCMNT 176
            |:  :  :::  ||   | | | ||||  : :  |          | ||||  |||||  :|
Db       29 APSPLPEVVGWDWEVKTNYAQFFRYLAQERCEVHRLGHSVEEAQKEHSKMQEIIAFKDLETLKRKY 94

Qy      177 LQCMNESGQLSLTMEPVKSSDKGIKPTFIEIVQSGAKTVDSRGGLFLDPHLVRGIEVTRCRGNQ 240
            |:|. |    :   :  |  ||||   :|   |: | | |      : : :   |
Db       95 LEGVPVPGQHQVPHMGIMIPVFSSQGECP   MSLEPHSGLTCEEK     KKLQAVKESLMHL 154

Qy      241 ATLTPVQAAN     KTCPTNYVWNNYMRCNTEAGQQDFTFYSNVEDDSINGFHIVCGPNK 296
            | | |    :     :||          |||                 |    |
Db      155 RPLTRRQTQHQVPRMGPQPRPC      RCRC                 RRFSFLRVCDSL 174

Qy      297 PTEDSQGF 304
            |. |||||
Db      175 LNNEDLCR 182


RESULT  13
VEGF_SHEEP
ID   VEGF_SHEEP     STANDARD;      PRT;   176 AA.
AC   P50412;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Ovis aries (sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Caprini; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97117954; PubMed=8968012;
RA   Ferrara N.A., Dai Y., Li B., Charnock-Jones D.S., Smith S.K.;
RA   Poyntkke D.P., Moar P.M.;
RT   "Characterization and expression of ovarian vascular endothelial growth
RT   factor (VEGF) in the ovine corpus luteum.";
RL   J. Reprod. Fertil. 108:157-165(1996).
CC   !  FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH, INDUCING ENDOTHELIAL CELL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   !  SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC   !  SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   !  SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X94596; CAA64277.1; -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD000629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00240; PDGF_1; 1.
DR   PROSITE; PS00278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL          1     26       BY SIMILARITY.
FT   CHAIN          27    136       VASCULAR ENDOTHELIAL GROWTH FACTOR
FT   DISULFID       51     93       BY SIMILARITY.
FT   DISULFID       82    127       BY SIMILARITY.
FT   DISULFID       89    129       BY SIMILARITY.
FT   DISULFID       76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID       85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD      103    103       N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ   SEQUENCE   136 AA;  15242 MW;  3E702A7B5A7F91/0 CRC64;

  Query Match             7.4%;  Score 173.5;  DB 1;  Length 136;
  Best Local Similarity   33.9%;  Pred. No. 5.5e-07;
  Matches   52;  Conservative   17;  Mismatches   42;  Indels   11;  Gaps    3;

Qy      113 EILKSIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQCMNTLQG 176
            :::| :|  :::: | | |  :|: :|:          |||  || : |||||| | |:: |
Db       38 EVMKFMDVYQRSYCHPIETLVEIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEES 99

Qy      177 LQCMNESGQLSLTMEPVKSSDKGIKPTFIEIVQSGAKTVDSRGGLFLDPHLVRGIEVTRCRGNQ 240
                  | |||:     :     :||  . | |  | |  ||
Db       97 EE        PNIIMQIMIIKPHQSQHIGEMSFLQHNKCECRPKKDRARQ 138


RESULT  14
VEGF_CHICK
ID   VEGF_CHICK     STANDARD;      PRT;   210 AA.
AC   P52870; Q91420;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Gallus gallus (chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Chicken; TISSUE=Heart;
RA   Takahashi T.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.c.japonica; TISSUE=Embryo;
RX   MEDLINE [illegible]; PubMed 7556[illegible];
RA   Flamme I., von Reutern M., Drexler H.C., Syed-Ali S., Risau W.;
RT   "Overexpression of vascular endothelial growth factor in the avian
RT   embryo induces hypervascularization and increased vascular
RT   permeability without alterations of embryonic pattern formation.";
RL   Dev. Biol. 171:399-414(1995).
RN   [3]
RP   SEQUENCE OF [illegible]-187 FROM N.A.
RC   SPECIES=C.c.japonica;
RX   MEDLINE [illegible]; PubMed 778[illegible];
RA   Flamme I., Breier G., Risau W.;
RT   "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT   (flk-1) are expressed during vasculogenesis and vascular
RT   differentiation in the quail embryo.";
RL   Dev. Biol. 169:699-712(1995).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS (VEGF 190, VEGF 166 AND VEGF
CC       146) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME
CC       GENE. THE LONGER FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL
CC       RETENTION SIGNAL.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY AND EQUALLY EXPRESSED IN HEART AND
CC       LIVER. IN KIDNEY, MUSCLE, BRAIN AND [illegible] VEGF 166 FORM IS
CC       5- TO 10- TIMES MORE ABUNDANT THAN THE VEGF 190 FORM.
CC   -!- DEVELOPMENTAL STAGE: THE VEGF 166 FORM IS EXPRESSED EARLY AT DAY 1
CC       AND IS [illegible] DURING GASTRULATION. EXPRESSION OF [illegible]
CC       FORM IS DETECTABLE ONLY FROM DAY 2.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AB011078; BAA24925.1; -.
DR   EMBL; S79680; AAB35371.1; -.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    216       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     83    128       BY SIMILARITY.
FT   DISULFID     87    13[illegible]       BY SIMILARITY.
FT   DISULFID     77     77       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     86     86       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    142    142       K -> N (IN ISOFORM VEGF 1[illegible]).
FT   VARSPLIC    143    16[illegible]       MISSING (IN ISOFORM VEGF 1[illegible]).
FT   VARSPLIC    166    166       F -> L (IN ISOFORM VEGF 1[illegible]).
FT   VARSPLIC    167    219       MISSING (IN ISOFORM VEGF 1[illegible]).
SQ   SEQUENCE   216 AA;  25[illegible] MW;  82E[illegible] CRC64;

  Query Match             7.4%;  Score 17[illegible];  DB 1;  Length 21[illegible];
  Best Local Similarity   22.1%;  Pred. No. 5.[illegible];
  Matches   46;  Conservative   38;  Mismatches   82;  Indels   12;  Gaps    8;

Qy        11[illegible] EILKSIDNEWRKT[illegible]MPREV[illegible]IDV[illegible]KEF[illegible]AAINIT[illegible]KP[illegible]VCVYR[illegible] 172
Db         [illegible] EVIKF[illegible] [illegible] 

Qy        173 SIGYLSKILFEIIVELS       [illegible]KPVIISFANHISC[illegible]MSKILVYEQVHSI[illegible]RESIPA 22[illegible]
Db         99 D--      -VYNVIMEIAKIKPHQ[illegible]HIAHMSF[illegible]QHSKC[illegible]RPKKIVENF[illegible]EKKSER[illegible]K 15[illegible]

Qy        228 [illegible]AANK[illegible]INVNNNY[illegible]NVE[illegible] [illegible]NKELIEI[illegible] 2[illegible]
Db        151 CQKKKKKKCRYKP[illegible]     SEH[illegible]SEKKHLFVQ          [illegible] 18[illegible]

Qy        287 CQCVCKGGIRPSSCGPHK ELDRDSCQC 313
Db        186 CK[illegible]SCK   EIDSP[illegible]KSRQLEINERI[illegible]R[illegible] 211


RESULT 15
NOTC_DROME
ID   NOTC_DROME     STANDARD;      PRT;  2703 AA.
AC   P07207; P04[illegible]4;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.
GN   N.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 860795[illegible]; PubMed 393[illegible];
RA   Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
RT   "Nucleotide sequence from the neurogenic locus notch implies a gene
RT   product that shares homology with proteins containing EGF-like
RT   repeats.";
RL   Cell 43:567-581(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OREGON R;
RX   MEDLINE 8701[illegible]624; PubMed 3097517;
RA   Kidd S., Kelley M.R., Young M.W.;
RT   "Sequence of the notch locus of Drosophila melanogaster: relationship
RT   of the encoded protein to mammalian clotting and growth factors.";
RL   Mol. Cell. Biol. 6:3094-3108(1986).
RN   [3]
RP   SEQUENCE OF 2505-2611 FROM N.A.
RX   MEDLINE 85099329; PubMed 2981631;
RA   Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
RT   "opa: a novel family of transcribed repeats shared by the Notch locus
RT   and other developmentally regulated loci in D. melanogaster.";
RL   Cell 40:55-62(1985).
RN   [4]
RP   SEQUENCE OF 1-8 FROM N.A.
RX   MEDLINE 87[illegible]7846; PubMed 303[illegible]327;
RA   Kelley M.R., Kidd S., Berg R.L., Young M.W.;
RT   "Restriction of P-element insertions at the Notch locus of Drosophila
RT   melanogaster.";
RL   Mol. Cell. Biol. 7:1545-1548(1987).
RN   [5]
RP   REVIEW.
RA   Harris W.A.;
RT   "Many cell types specified by Notch function.";
RL   Curr. Biol. 1:120-122(1991).
CC   -!- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION OF
CC       ECTODERM.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
CC       THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
CC       DEVELOPMENT IN INSECTS. THIS PROCESS IS UNDER CONTROL OF THE
CC       NEUROGENIC GENES.
CC   -!- SIMILARITY: HIGH, WITH OTHER NOTCH TYPE PROTEINS.
CC   -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC   -!- SIMILARITY: CONTAINS 6 ANK REPEATS.
```

```
DR   EMBL; M16152; AAB59220.1; -.
DR   EMBL; M16153; AAB59220.1; JOINED.
DR   EMBL; M16149; AAB59220.1; JOINED.
DR   EMBL; M16150; AAB59220.1; JOINED.
DR   EMBL; M16151; AAB59220.1; JOINED.
DR   EMBL; K03508; AAA28725.1; -.
DR   EMBL; M13689; AAA28725.1; JOINED.
DR   EMBL; K03507; AAA28725.1; JOINED.
DR   EMBL; M12175; AAA74496.1; -.
DR   EMBL; M16025; AAA28726.1; -.
DR   PIR; A24420; A24420.
DR   PIR; A24768; A24768.
DR   PIR; A05267; A05267.
DR   HSSP; P00740; 1IXA.
DR   FlyBase; FBgn0004647; N.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000152; Asx hydroxyl.
DR   InterPro; IPR000561; EGF like.
DR   InterPro; IPR000742; EGF 2.
DR   InterPro; IPR001881; EGF Ca.
DR   InterPro; IPR001438; EGF II.
DR   InterPro; IPR000800; Notch.
DR   Pfam; PF00023; ank; 6.
DR   Pfam; PF00008; EGF; 36.
DR   Pfam; PF00066; notch; 3.
DR   PRINTS; PR00010; EGFBLOOD.
DR   SMART; SM00248; ANK; 4.
DR   SMART; SM00179; EGF CA; 23.
DR   SMART; SM00181; EGF like; 13.
DR   SMART; SM00004; NL; 2.
DR   PROSITE; PS50088; ANK REPEAT; 5.
DR   PROSITE; PS50297; ANK REP REGION; 1.
DR   PROSITE; PS00010; ASX HYDROXYL; 22.
DR   PROSITE; PS00022; EGF 1; 34.
DR   PROSITE; PS01186; EGF 2; 28.
DR   PROSITE; PS01187; EGF CA; 22.
KW   Differentiation; Neurogenesis; Repeat; ANK repeat; EGF like domain
KW   Transmembrane; Signal; Glycoprotein.
FT   SIGNAL        1     44       POTENTIAL.
FT   CHAIN        45   2703       NEUROGENIC LOCUS NOTCH PROTEIN
FT   DOMAIN       45   1745       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1746   1766       POTENTIAL.
FT   DOMAIN     1767   2703       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       58     95       EGF LIKE 1.
FT   DOMAIN       96    136       EGF LIKE 2.
FT   DOMAIN      139    176       EGF LIKE 3.
FT   DOMAIN      177    215       EGF LIKE 4.
FT   DOMAIN      217    253       EGF LIKE 5, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      255    291       EGF LIKE 6.
FT   DOMAIN      293    329       EGF LIKE 7, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      331    370       EGF LIKE 8, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      372    408       EGF LIKE 9, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      409    447       EGF LIKE 10.
FT   DOMAIN      449    486       EGF LIKE 11, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      488    524       EGF LIKE 12, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      526    562       EGF LIKE 13, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      564    600       EGF LIKE 14, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      602    637       EGF LIKE 15, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      639    675       EGF LIKE 16, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      677    713       EGF LIKE 17, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      715    751       EGF LIKE 18, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      753    789       EGF LIKE 19, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      791    827       EGF LIKE 20, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      829    865       EGF LIKE 21, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      867    905       EGF LIKE 22.
FT   DOMAIN      907    944       EGF LIKE 23, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      946    982       EGF LIKE 24, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN      984   1020       EGF LIKE 25.
FT   DOMAIN     1022   1058       EGF LIKE 26, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN     1060   1096       EGF LIKE 27.
FT   DOMAIN     1099   1134       EGF LIKE 28.
FT   DOMAIN     1136   1181       EGF LIKE 29.
FT   DOMAIN     1183   1219       EGF LIKE 30, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN     1221   1257       EGF LIKE 31, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN     1259   1295       EGF LIKE 32, CALCIUM BINDING (POTENTIAL).
FT   DOMAIN     1297   1335       EGF LIKE 33.
FT   DOMAIN     1337   1373       EGF LIKE 34.
FT   DOMAIN     1375   1412       EGF LIKE 35.
FT   DOMAIN     1415   1451       EGF LIKE 36.
FT   REPEAT     1475   1513       LIN/NOTCH 1.
FT   REPEAT     1514   1553       LIN/NOTCH 2.
FT   REPEAT     1554   1593       LIN/NOTCH 3.
FT   REPEAT     1901   1945       ANK 1.
FT   REPEAT     1950   1979       ANK 2.
FT   REPEAT     1983   2013       ANK 3.
FT   REPEAT     2017   2046       ANK 4.
FT   REPEAT     2050   2079       ANK 5.
FT   REPEAT     2083   2112       ANK 6.
FT   DOMAIN     2538   2569       POLY-GLN (OPA REPEAT).
FT   DISULFID     62     73       BY SIMILARITY.
FT   DISULFID     67     83       BY SIMILARITY.
FT   DISULFID     85     94       BY SIMILARITY.
FT   DISULFID    100    111       BY SIMILARITY.
FT   DISULFID    105    124       BY SIMILARITY.
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FT   DISULFID    181    192       BY SIMILARITY.
FT   DISULFID    186    203       BY SIMILARITY.
FT   DISULFID    205    214       BY SIMILARITY.
FT   DISULFID    221    232       BY SIMILARITY.
FT   DISULFID    226    241       BY SIMILARITY.
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FT   DISULFID    297    308       BY SIMILARITY.
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FT   DISULFID    398    407       BY SIMILARITY.
FT   DISULFID    413    424       BY SIMILARITY.
FT   DISULFID    418    435       BY SIMILARITY.
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FT   DISULFID    453    465       BY SIMILARITY.
FT   DISULFID    459    474       BY SIMILARITY.
FT   DISULFID    476    485       BY SIMILARITY.
FT   DISULFID    492    503       BY SIMILARITY.
FT   DISULFID    497    512       BY SIMILARITY.
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FT   DISULFID    535    550       BY SIMILARITY.
FT   DISULFID    552    561       BY SIMILARITY.
FT   DISULFID    568    579       BY SIMILARITY.
FT   DISULFID    573    588       BY SIMILARITY.
FT   DISULFID    590    599       BY SIMILARITY.
FT   DISULFID    606    616       BY SIMILARITY.
FT   DISULFID    611    625       BY SIMILARITY.

  Query Match             7.0%;  Score 163;  DB 1;  Length 2703;
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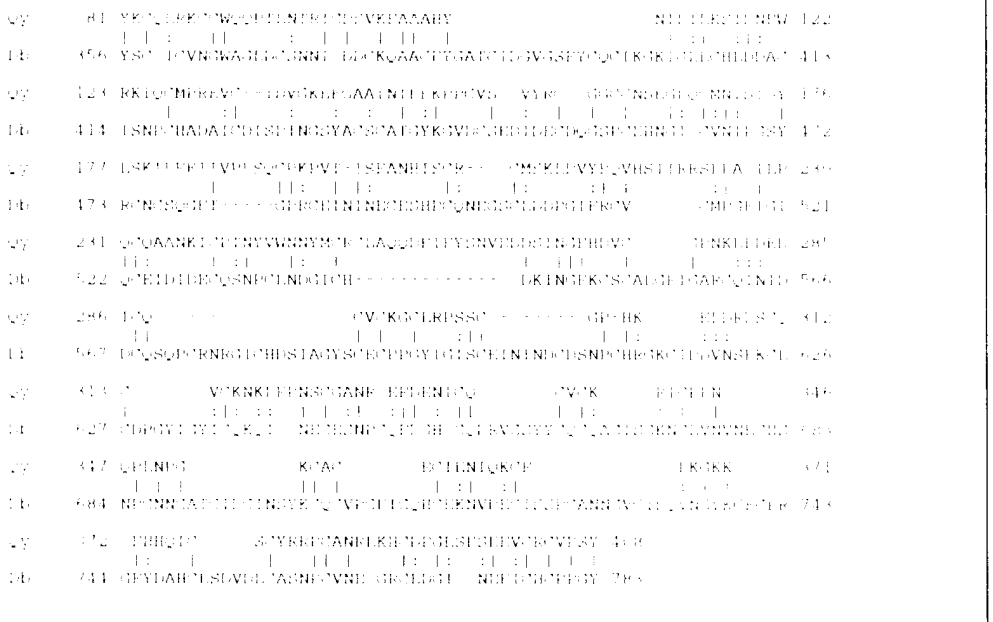


Search completed: February 20, 2002, 16:27:32
Job time: 170 sec

SW protein - protein search, using sw model

Run on: February 20, 2002, 16:20:52 ; Search time 27.95 Seconds
(without alignments)
1222.918 Million cell updates/sec

Title: US-09-534-376A-11
Perfect score: 2338
Sequence: 1 MRLLCFLSLACSLLAAALIP.....SPSEEVCPGVPGVWKRSSRLN 419

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

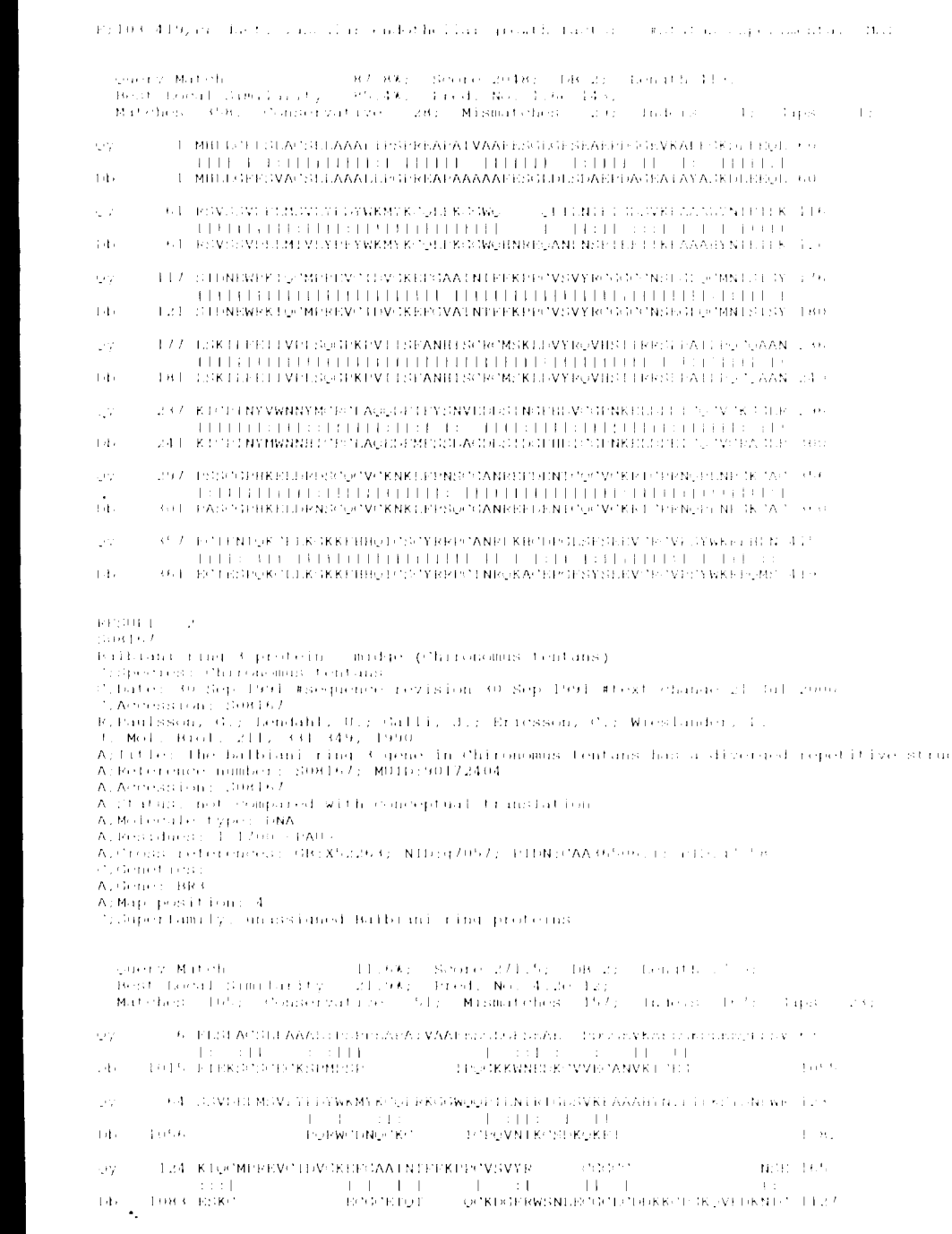
Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2048	87.8	419	2	S69207	vascular endotheli
2	271.5	11.6	1288	2	S38167	fibrinol ritus 1 pr
3	232	9.9	232	2	A41551	vascular endothelI
4	211.5	9.1	190	2	S52130	vascular endotheli
5	201.5	8.6	190	2	A35987	glioma derived vas
6	200.5	8.6	190	2	B44881	vascular endotheli
7	198.5	8.5	190	2	B40080	vascular endotheli
8	195.5	8.4	214	2	A44881	vascular endotheli
9	190.5	8.2	473	2	A56175	adhesion plaque pr
10	181	7.8	160	2	JQ0542	1958 secretory pro
11	179.5	7.7	188	2	JC4680	vascular endotheli
12	176.5	7.6	2352	2	I30201	Notch homolog prot
13	174.5	7.4	146	2	S57956	c-fms vascular end
14	172.5	7.4	120	2	A33787	vascular endotheli
15	170	7.3	2471	2	A49128	cell-fate determin
16	167	7.2	1203	2	A49175	Notch 3 protein -
17	163	7.0	2703	1	A24420	notch protein - fr
18	161.5	6.9	1964	2	I09054	notch1 - mouse
19	160	6.9	148	2	D49530	1-K vascular endot
20	159.5	6.8	133	2	B49539	vascular endotheli
21	159.5	6.8	4645	2	I10053	laminin alpha 5 ch
22	157	6.7	1372	2	I25933	hypothetical prote
23	154.5	6.6	149	2	A41236	placental growth f
24	153.5	6.6	2555	2	A40043	notch protein homo
25	151.5	6.5	2437	2	S42612	transmembrane prot
26	151.5	6.5	3002	2	A47221	fibrillin 1 precur
27	151	6.5	4672	2	I23433	hypothetical prote
28	151	6.5	4704	2	I47316	probable laminin a
29	150.5	6.5	565	2	I16408	hypothetical prote
30	149	6.4	1557	2	I28811	hypothetical prote
31	148	6.3	1220	2	A56136	jagged protein pre
32	148	6.3	2139	2	A55672	crumbs protein - f
33	147.5	6.3	1810	1	A42250	tenascin precursor
34	147.5	6.3	2524	2	A55844	Xotch protein - Af
35	147.5	6.3	2531	2	A49019	Notch 1 protein
36	147.5	6.3	2871	2	A55567	fibrillin 1 - bova
37	147	6.3	207	2	JC4679	vascular endotheli
38	146.5	6.3	1790	1	MMFFB1	laminin beta 1 cha
39	146.5	6.3	2195	2	I44264	hypothetical prote
40	146	6.3	2871	2	A55624	fibrillin 1 precur
41	145.5	6.2	798	2	A28193	integrin beta 1 ch
42	145.5	6.2	1429	2	S30434	homeotic protein 1
43	145.5	6.2	2907	2	A57278	fibrillin 2 precur
44	145.5	6.2	2918	2	A54105	fibrillin 2 precur
45	145	6.2	1680	2	A43434	furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand; DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A;Reference number: S69207; MUID:96203094
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:g227096; PIDs:g118
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4
A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 70-419 <JOU>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X',104-126 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:g1473426; PIDN:AAB02909.1; PID:g1473427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:489088; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>



RESULT 1
A41951
Vascular endothelial growth factor 206 precursor - human
N;Alternate names: vascular permeability factor
N;Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VE
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1992 #sequence_revision 28-Apr-1992 #text_change 05-Nov-1999
C;Accession: A41951; G41951; B41951; A40454; B40454; G40454; A40679; A40680; D41951;
R;Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A;Title: The vascular endothelial growth factor family: identification of a fourth mo
A;Reference number: A41951; MUID:92106017
A;Accession: A41951
A;Molecule type: mRNA
A;Residues: 1-232 <HOU>
A;Cross-references: GB:S67192; NID:g246155; PID:g246156
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-140,'N',183-232 <HOU>
A;Accession: B41951
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-141,227-232 <HOU>
R;Fischer, E.; Mitchell, R.; Bartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;
J. Biol. Chem. 266, 11947-11954, 1991
A;Title: The human gene for vascular endothelial growth factor. Multiple protein f
A;Reference number: A40454; MUID:91268072
A;Accession: A40454
A;Molecule type: DNA
A;Residues: 1-195,183-232 <FIS>
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A;Molecule type: DNA
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A;Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;
Keyt, B.A.; Nguyen, T.; Berleau, L.; Chen, H.; Weiler, S.; Watson, T.J.; Fedder, J.;
Science 246, 1309-1312, 1989
A;Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A;Reference number: A40679; MUID:90069609
A;Accession: A40679
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-165,183-232 <KEY>
A;Cross-references: GB:M27281; NID:g340300; PID:AAA36897.1; PID:g340301
R;Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A;Title: Vascular endothelial growth factor is a secreted angiogenic mitogen

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A;Reference number: A4[illegible]80; MUID:[illegible]
A;Accession: A[illegible]80
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14[illegible],'N',183-232 <TED>
A;Cross-references: GB:M32977; NID:g181970; PIDN:AAA[illegible]; PID:g[illegible]
R;Weindel, K.; Marme, D.; Weich, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A;Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial
A;Reference number: JQ1463; MUID:92231879
A;Accession: JQ1463
A;Molecule type: mRNA
A;Residues: 1-14[illegible],'N',183-232 <WEI>
A;Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
A;Experimental source: AIDS Kaposi's sarcoma cell
A;Accession: JQ1464
A;Molecule type: mRNA
A;Residues: 1-140,'N',227-232 <WE2>
A;Experimental source: AIDS Kaposi's sarcoma cell
R;Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay
J. Biol. Chem. 264, 20017-20024, 1989
A;Title: Human vascular permeability factor. Isolation from [illegible] cells.
A;Reference number: A34492; MUID:[illegible]2112
A;Accession: A34492
A;Molecule type: protein
A;Residues: 27-[illegible];43-49,'R';72-76,'Q',78-81;[illegible] <CON>
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A;Gene: GDB:VEGF
A;Cross-references: GDB:132244; OMIM:192240
A;Map position: 6p21-6p12
C;Function:
A;Description: promotes fluid and protein leakage from blood vessels
C;Keywords: alternative splicing; angiogenesis; dimer; [illegible] extracellular pr
F;1-232/Product: vascular endothelial growth factor 2[illegible] precursor #status predicted <VZ
F;1-165,183-232/Product: vascular endothelial growth factor 1[illegible] precursor #status predic
F;1-141,227-232/Product: vascular endothelial growth factor 1[illegible] precursor #status predi
F;1-26/Domain: signal sequence #status predicted <SIG>
F;[illegible]/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             [illegible]%;  Score 231;  DB 2;  Length [illegible];
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  Matches   63;  Conservative   30;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy    113 EIIKSIDNEWRKIQCMPREV[illegible]VGKEFGAAINIFFKPP[illegible] 172
Db     [illegible] EVVKFMDVYQRSY[illegible]VDIFQEYPDEIEYIFKPS[illegible]VPLMR[illegible]

Qy    173 SIGYLSKILEEIIVPLSQGPKPVIISFANHISCRCMSKLDVYRQVHSIIRR[illegible] 2[illegible]
Db     [illegible] EESNITMQIMRIKP[illegible]HIGEMSFLQHNKCE[illegible]KKDRARQEKK[illegible]

Qy    2[illegible] QAANKTCPTNYVWNNYM[illegible]CRAQQDFIFYSNVEDDSINGFHDV[illegible]ENKF[illegible] 2[illegible]
Db    151 QKRKRKKSRYKSWSVYVGARC[illegible]                       [illegible]M [illegible]

Qy    2[illegible] K[illegible]RPSS[illegible]PHKE       [illegible]RSGQ[illegible]VCKNKLFPNS[illegible]ANR[illegible] 3[illegible]
Db    1[illegible] PW[illegible]HRCPS[illegible]ERRKHLFVQDPQ[illegible]K[illegible]KNT[illegible]KARQLELNERTCR[illegible] 2[illegible]

RESULT 4
S52130
vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change [illegible]
C;Accession: S52130
R;Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Nucleotide sequence and expression of the porcine vascular endothelial growth f
A;Reference number: S52130; MUID:95143284
A;Accession: S52130
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81380; NID:g[illegible]; PIDN:CAA[illegible]; PID:g[illegible]

  Query Match             [illegible]%;  Score 211.5;  DB 2;  Length 190;
  Best Local Similarity   24.8%;  Pred. No. 1.2e-08;
  Matches   58;  Conservative   24;  Mismatches   57;  Indels   95;  Gaps   [illegible];

Qy    113 E[illegible]IKSIDNEWRKIQCMPREV[illegible]VGKEFGAAINIFFKPP[illegible]MN[illegible] 172
Db     38 EVVKFMDVYQRSYCRPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPT 96

Qy    173 SIGYLSKILEEIIVPL       SQGPKPVIISFANHISCRCMSKLDVYRQVHSIIRR[illegible]A 227
Db     97 EE         ENITMQIMRIKPHQSQHIGEMSFLQHNKCECRPKKDRARQ             138

Qy    228 [illegible]QAANKTCPTNYVWNNYM[illegible]CRAQQDFIFYSNVEDDSINGFHDV[illegible]ENKF[illegible] 287
Db    139    ---  --         -        --       ENP[illegible]SE      14[illegible]

Qy    288 Q[illegible]VCK[illegible]RLRPSS[illegible]PHKEL[illegible]RESGQ[illegible]VCKNKLFPNS[illegible]ANR[illegible]ENT[illegible] 3[illegible]
Db    148          KKKHLFVQDPQTCKCSCKNT[illegible]DSRCKARQLELNERTCRC 185

RESULT 5
A35987
glioma-derived vascular endothelial cell growth factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 05-Nov-1999
C;Accession: A35987
R;Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; He
Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990
A;Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is
A;Reference number: A35987; MUID:[illegible]249
A;Accession: A35987
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <CON>
A;Cross-references: GB:M32167; NID:g204287; PIDN:AAA41211.1; PID:g204288

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  Best Local Similarity   2[illegible]%;  Pred. No. [illegible]e-08;
  Matches   [illegible];  Conservative   [illegible];  Mismatches   74;  Indels   [illegible];  Gaps   [illegible];

Qy     85 LRK[illegible]VKEAAAG[illegible]NEWRKI[illegible]CMPREV[illegible]AAI 144
Db     18 LHHAKWSQAAPTT[illegible]    KAH    EVVKFMDVYQRSY[illegible]VDIFQEYPDE[illegible]

Qy    145 NIFFKPP[illegible]VSVYR[illegible]MNI[illegible]SKILEEIIVPLSQ[illegible]GPKPVIISFANH 202
Db     69 EYIFKPSCVPLMRCA[illegible]NEEALE[illegible]VPTSESNVIMQIMRIKPHQSQHIG    EMSFLQH 1[illegible]4

Qy    203 ISCRCMSKLDVYRQVHSIIRR[illegible]QAANKTCPTNYVWNNYM[illegible]CRAQQDFIFY [illegible]
Db    125 SKCECRPKKD --       -              RTKPENH       [illegible]SEKKKHLFV 1[illegible]4

Qy    262 SNVEDDSINGFHDV[illegible]ENKF[illegible]Q[illegible]VCKGGLRPSS[illegible]PHK ELF[illegible] 3[illegible]
Db    155 Q                       DPQ[illegible]CKCSCKN  TDSRCKARQLELNERTCRC 1[illegible]

RESULT 6
B44881
vascular endothelial growth factor 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision [illegible]-Feb-1994 #text_change [illegible]-Nov-1999
C;Accession: B44881; A4[illegible]; A[illegible]
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, [illegible], 1992
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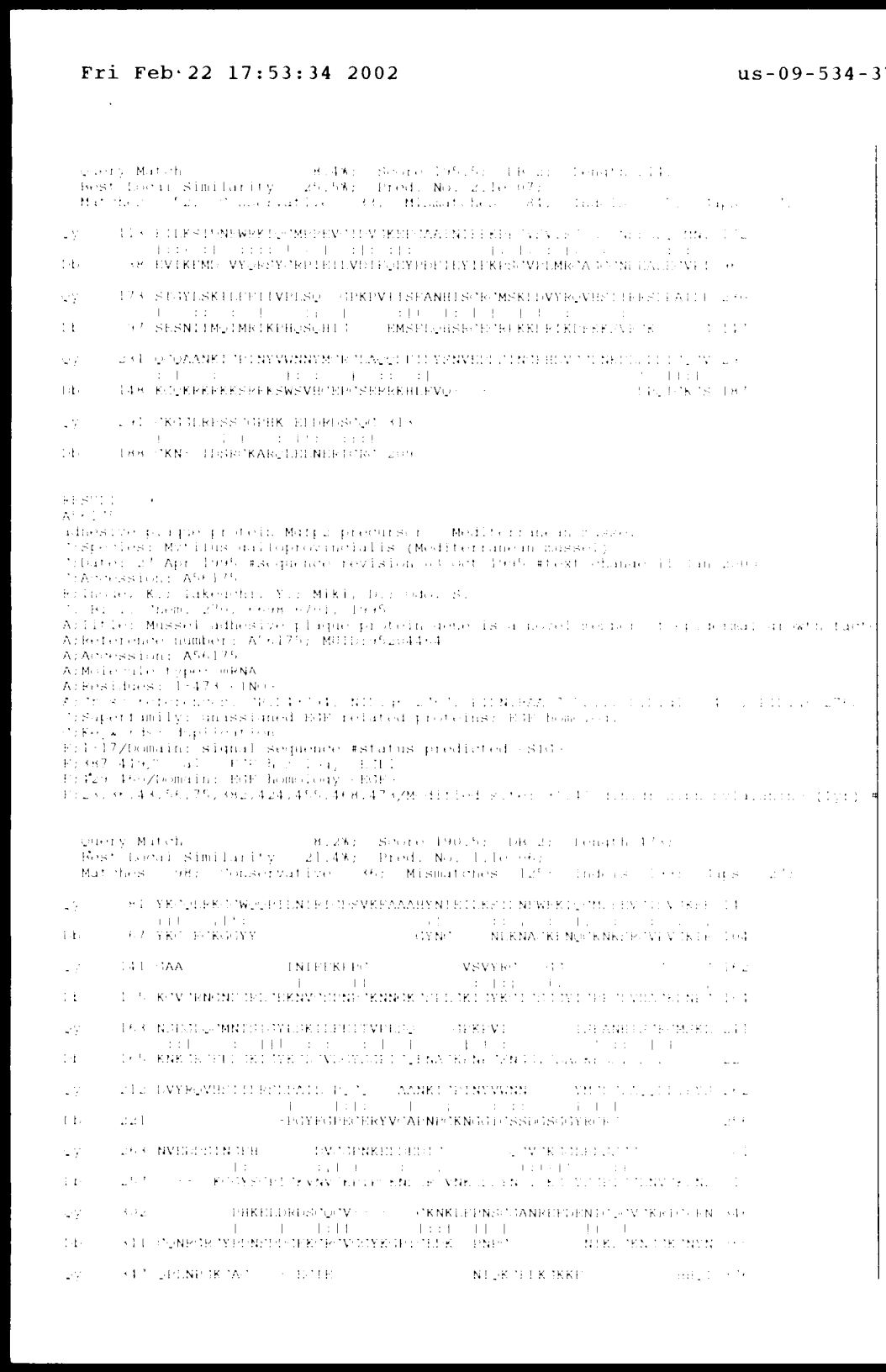
A;Title: Expression of vascular endothelial growth factor [illegible]
A;Reference number: A44081; MUID:92274860
A;Accession: B44081
A;Molecule type: mRNA
A;Residues: 1-214 <BEE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22254.1; PID:g249857
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:164774, NCBIP:164778)
R;Claesson, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endot
A;Reference number: A00932; MUID:91079779
A;Accession: A00932
A;Molecule type: protein
A;Residues: 1-85 <CLA>
R;Senthana, L.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1221, 69-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous
A;Reference number: S52196; MUID:95101726
A;Accession: S52196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-45 <SEN>
C;Comment: Residues could be demonstrated for recombinant VEGF 2 but 1 VEGF s
C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodim
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor 3 #status experimental <MAT>

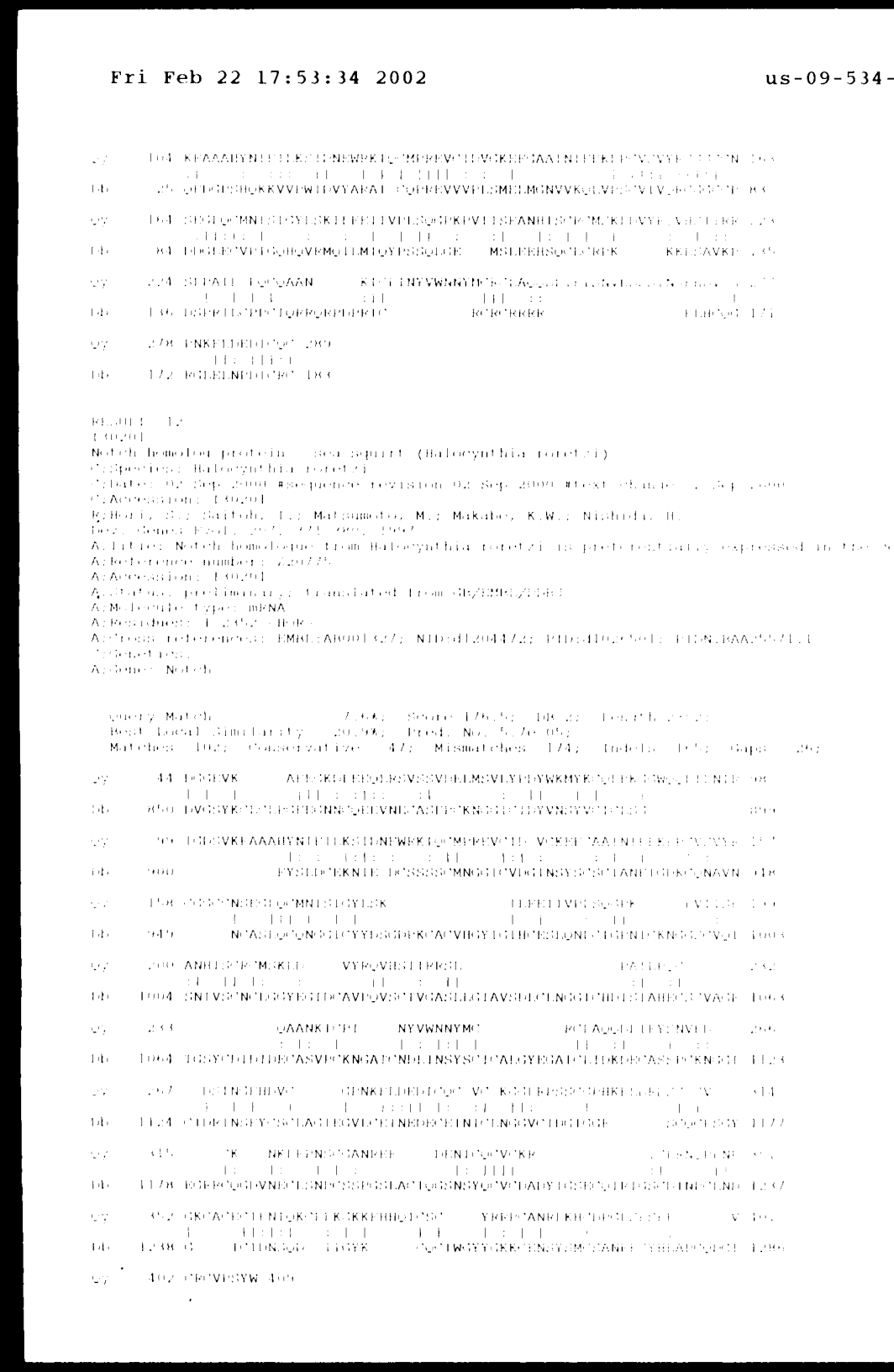
A;Reference number: A44081; MUID:92274860
A;Accession: A44081
A;Molecule type: mRNA
A;Residues: 1-214 <BEE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22254.1; PID:g249857
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:164774, NCBIP:164778)
A;Accession: B44081
A;Molecule type: mRNA
A;Residues: 1-140,209-214 <BEE>
A;Cross-references: GB:S37052; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:167024, NCBIP:167026)
R;Claesson, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endot
A;Reference number: A00932; MUID:91079779
A;Accession: A00932
A;Molecule type: protein
A;Residues: 1-85 <CLA>
R;Senthana, L.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1221, 69-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous
A;Reference number: S52196; MUID:95101726
A;Accession: S52196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-45 <SEN>
C;Comment: Residues could be demonstrated for recombinant VEGF 2 but 1 VEGF s
C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodim
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor 3 #status experimental <MAT>

RESULT 8
A44081
vascular endothelial growth factor 3 precursor - mouse
N;Contains: vascular endothelial growth factor 2; vascular permeability factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: A44081; C44081; A00932; S52196
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogeneto
A;Reference number: A44081; MUID:92274860
A;Accession: A44081
A;Molecule type: mRNA
A;Residues: 1-214 <BEE>
A;Cross-references: GB:S37052; NID:g249856; PIDN:AAB22254.1; PID:g249857
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:164774, NCBIP:164778)
A;Accession: C44081
A;Molecule type: mRNA
A;Residues: 1-140,209-214 <BEE>
A;Cross-references: GB:S37052; NID:g249860; PIDN:AAB22254.1; PID:g249861
A;Note: sequence extracted from NCBI backbone (NCBIN:167024, NCBIP:167026)
R;Claesson, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.
J. Exp. Med. 172, 1535-1545, 1990
A;Title: Vascular permeability factor: a tumor-derived polypeptide that induces endot
A;Reference number: A00932; MUID:91079779
A;Accession: A00932
A;Molecule type: protein
A;Residues: 1-85 <CLA>
R;Senthana, L.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.
Biochim. Biophys. Acta 1221, 69-370, 1994
A;Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous
A;Reference number: S52196; MUID:95101726
A;Accession: S52196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-45 <SEN>
C;Comment: Residues could be demonstrated for recombinant VEGF 2 but 1 VEGF s
C;Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodim
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-214/Product: vascular endothelial growth factor 3 #status experimental <MAT>



RESULT 10
JQ0542
185K secretory protein - mouse (Chrysomys tentans) (fragment)
N;Alternate names: balbiani ring 3 protein
C;Species: Chrysomys tentans
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 17-Mar-2000
C;Accession: JQ0542
R;Hignam, S.S.; Case, S.I.
Gene 88, 143-148, 1990
A;Title: Balbiani ring 3 in Chrysomys tentans encodes a 185 kDa secretory pr
A;Reference number: JQ0542; MUID:90206900
A;Accession: JQ0542
A;Molecule type: mRNA
A;Residues: 1-160 <DIG>
A;Cross-references: GB:M24160
A;Experimental source: salivary gland
C;Superfamily: unassigned Balbiani ring proteins

RESULT 11
JC4680
vascular endothelial growth factor related factor 167 precursor - mouse
N;Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 10-May-1996 #text_change 05-Nov-1999
C;Accession: JC4680
R;Clownson, S.; Lapeterantz, L.; Grimmond, S.; Stilins, S.; Nordonskjeld, M.; Weber, P
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A;Title: Characterization of the murine VEGF related factor gene
A;Reference number: JC4680; MUID:96298052
A;Accession: JC4680
A;Molecule type: mRNA
A;Residues: 1-188 <DOW>
A;Cross-references: GB:U43368; NID:g1256777; PID:g1256778
C;Comment: This factor is a mitogen that is selective for endothelial cells, and bot
at endothelial growth factors 167 and VEGF 186.
C;Genetics:
A;Gene: vrf
A;Map position: 19
A;Introns: 147/2
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-209/Product: vascular endothelial growth factor related fact 1 #status predicted

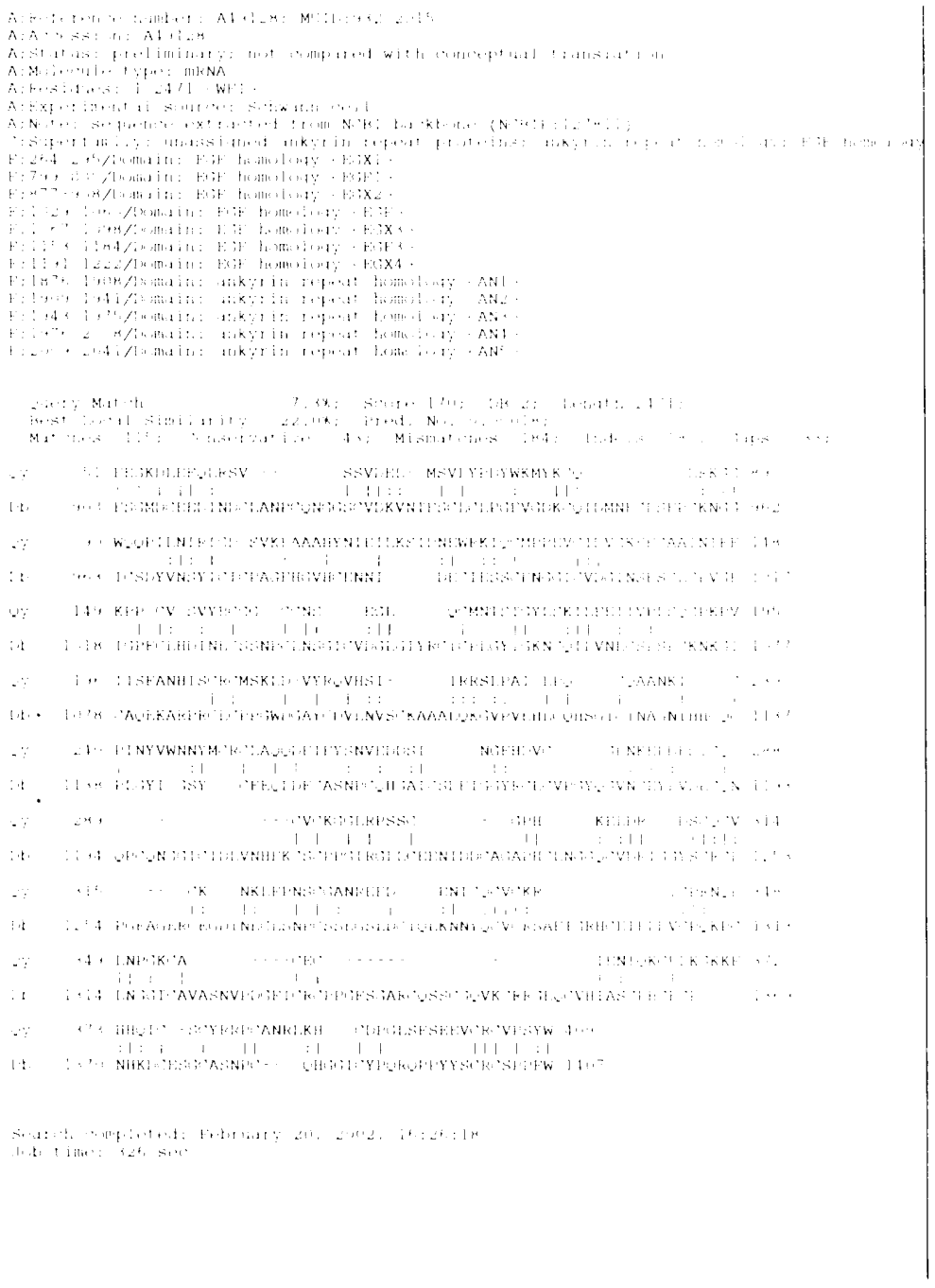


RESULT 12
I30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: I30201
R;Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 441-449, 1998
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the ne
A;Reference number: Z20177
A;Accession: I30201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2452 <HOR>
A;Cross-references: EMBL:AB001427; NID:g12044722; PID:g12044723; PID:g3550151; PIDN:BAA33711.1
C;Genetics:
A;Gene: Notch

RESULT 13
S57956
ovine vascular endothelial growth factor - sheep
C;Species: ovis orientalis aries, ovis ammon aries (domestic sheep)
C;Date: 31-Jan-1995 #sequence_revision 31-Jan-1995 #text_change 05-Nov-1999
C;Accession: S57956
R;Redmer, D.A.; Doraiswamy, V.; Bortnem, B.J.; Jones, S.C.; Moore, K.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S57956
A;Accession: S57956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X86406; NID:g899487; PIDN:CAA60277.1; PID:g899488

RESULT 14
A33787
vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 09-Nov-1999
C;Accession: A33787
R;Fischer, R.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet derived gro
A;Reference number: A33787; MUID:90012225
A;Accession: A33787
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <FIS>
A;Cross-references: GB:M32250; NID:g163810; PIDN:AAA30805.1; PID:g165811
C;Keywords: alternative splicing

RESULT 15
A49128
cell fate determining gene Notch2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 15-Aug-1997
C;Accession: A49128
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 931-941, 1991
A;Title: Notch2: a second mammalian Notch gene.



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

M protein - protein search, using sw model

Run on: February 20, 2002, 16:20:31 ; Search time 1.00 Seconds
(without alignments)
725.694 Million cell updates/sec

Title: US-09-534-376A-11
Perfect score: 2333
Sequence: 1 MRILQFLSLACSLIAAALIP.....SFSEEVQPVSVYWKSFQN 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 740743290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/geneseq/g_biosci_v:AAB*.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2333	100.0	419	19	AAW75742	Mouse vascular endothelial growth factor C protein.
2	2308	98.8	419	18	AAW75739	Mouse VEGF-C protein.
3	2048	87.8	419	18	AAW17887	Human fetal liver vascular endothelial growth factor VEGF-C.
4	2048	87.8	419	18	AAW60952	Human fetal neoplastic vascular endothelial growth factor VEGF-C.
5	2048	87.8	419	19	AAW75740	Human vascular endothelial growth factor VEGF-C protein.
6	2048	87.8	419	20	AAW86233	Human vascular endothelial growth factor VEGF-C.
7	2048	87.8	419	21	AAB10648	Human VEGF protein.
8	2048	87.8	419	21	AAB29048	Human VEGF-C protein.
9	2048	87.8	419	21	AAY72747	Human prepro vascular endothelial growth factor VEGF-C.
10	2048	87.8	419	21	AAY79982	Human vascular endothelial growth factor VEGF-C.
11	2048	87.8	419	22	AAB37605	Human VEGF-C.
12	2039	87.4	419	18	AAW14833	Human vascular endothelial growth factor VEGF-C.
13	2038	87.4	419	20	AAY39518	Vascular endothelial growth factor VEGF-C.
14	2038	87.4	419	20	AAY22320	Full length human vascular endothelial growth factor VEGF-C.
15	2038	87.4	419	21	AAY97144	Vascular endothelial growth factor VEGF-C.
16	2038	87.4	419	22	AAY47570	Human VEGF-C protein.
17	2037	87.3	419	19	AAW75741	Vascular endothelial growth factor VEGF-C.
18	2035	87.2	419	18	AAW11478	Human vascular endothelial growth factor VEGF-C.
19	1909	84.4	409	20	AAW86237	Human VEGF-C full length protein.
20	1788	76.4	450	20	AAY80519	A truncated vascular endothelial growth factor VEGF-C.
21	1788	76.4	450	20	AAY22421	Truncated human VEGF-C protein.
22	1788	76.4	450	21	AAY97145	Truncated vascular endothelial growth factor VEGF-C.
23	1788	76.4	450	22	AAY97572	Human VEGF-C protein.
24	1778	76.2	450	20	AAB82686	Vascular endothelial growth factor VEGF-C.
25	1747.5	74.9	418	18	AAW00454	Full length VEGF-C protein.
26	1747.5	74.9	418	19	AAW75743	Full length vascular endothelial growth factor VEGF-C.
27	1658	71.1	418	20	AAY98284	Human VEGF-C with tag.
28	1621	69.5	407	20	AAW86222	Human VEGF-C truncated protein.
29	1590	68.2	402	20	AAW86223	Human VEGF-C truncated protein.
30	1569	67.3	397	20	AAW86224	Human VEGF-C truncated protein.
31	1546	66.3	392	20	AAW86225	Human VEGF-C truncated protein.
32	696	29.8	454	19	AAW40066	Human growth arrest specific protein 1.
33	696	29.8	454	19	AAW63241	Homo sapiens vascular endothelial growth factor VEGF-C.
34	696	29.8	454	19	AAW44293	Human vascular endothelial growth factor VEGF-C.
35	696	29.8	454	21	AAB10049	Human VEGF-C protein.
36	696	29.8	454	21	AAB29049	Human VEGF-C protein.
37	696	29.8	454	21	AAY70750	Human prepro vascular endothelial growth factor VEGF-C.
38	696	29.8	454	21	AAY70983	Human vascular endothelial growth factor VEGF-C.
39	696	29.8	454	22	AAY97573	Human VEGF-DI protein.
40	696	29.8	454	22	AAB37606	Human VEGF-D.
41	695.5	29.8	425	19	AAW55240	Homo sapiens vascular endothelial growth factor VEGF-C.
42	695.5	29.8	425	22	AAY97572	Human VEGF-C protein.
43	695.5	29.8	425	21	AAY98284	Human growth factor protein.
44	695.5	29.8	425	20	AAW14962	Marine-derived EGF-like protein.
45	695.5	29.8	425	19	AAW75742	Mus musculus vascular endothelial growth factor VEGF-C.

ALIGNMENTS

RESULT 1
AAW75742
ID AAW75742 standard; protein; 419 AA.
XX
AC AAW75742;
XX
DT 31-DEC-1999 (first entry)
XX
DE Mouse vascular endothelial growth factor C protein.
XX
KW VEGF; vascular endothelial growth factor C; vascular endothelial
KW receptor; cell function; cell proliferation; anti-psoriatic;
KW lymphatic disorder; oedema; cephalization; Milroy's disease.
XX
OS Mus sp.
XX
PN WO9943817-A1.
XX
PD 06-AUG-1999.
XX
PF 02-FEB-1999; 99WO-US002143.
XX
PR 05-FEB-1998; 98US-0074046.
XX
PA (UJHW-) UNIV HELSINKI LICENSING LTD.
XX
PI Alitalo K, Jeltsch V;
XX
DR WPI; 1999-514747/43.
DR N-PSDB; AAV52977.
XX
PT New isolated vascular endothelial growth factor polypeptide(s)
PT used to develop products for treating, e.g. cancers, inflammation.

```
PT   oedema, thrombocytopenia or for wound healing or tissue
PT   transplantation
XX
PS   Example 20; Page 117; 177pp; English.
XX
CC   The vascular endothelial growth factor C (VEGF C) polypeptides have
CC   activities affecting growth and migration of vascular endothelial cells,
CC   promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC   increasing vascular permeability, and affecting myelopoiesis. The
CC   products can be used for stimulating angiogenesis, for inhibiting
CC   angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC   of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC   also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC   They can also be used for modulating the growth of endothelial cells.
CC   They can also be used to stimulate lymphocyte production and maturation,
CC   and to promote or inhibit trafficking of lymphocytes between tissues and
CC   lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ   Sequence  415 AA;


  Query Match             100.0%;  Score 2433;  DB 16;  Length 415;
  Best Local Similarity   100.0%;  Pred. No. 0.4e-174;
  Matches  415;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MHLLGFFSVACSLLAAALLPGPREAPAIVAAPESGLGFSEAEPHGCHVKAFEGKDLEEGA 60
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Db       1 mhllgffsiacsllaaallpgpreapaivaapesglgfseaephgchvkafegkdleega 60

Qy      61 RSVSSVDELMSVLYPDYWKMYKCQLRKGGWQHNREQVNLNSRTKETIKFAAAHYNTEILKSID 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rsvssvdelmsvlypdywkmykcqlrkggwqhnreqvnlnsrtketikfaaahyntеilksid 120

Qy     121 EWRKTQMMPREVMDVGKEFGAATNTFKPPSVVSVYRCGGVCNSEGLQCMNTSTGYLSKT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ewrktqmmprevmdvgkefgaatntfkppsvvsvyrcggvcnsegLqcmntstgylskt 180

Qy     181 LFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCP 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lfeitvplsqgpkpvtistanhtscrcmskldvyrqvhsiirrslpatlpqcqaankTcp 240

Qy     241 TNYVWNNYMCRCLAQQDFIFYSNVEDWGSNGFHDVCQPNKELDEWCDRVCKSIDMVSSN 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 tnyvwnnymcrclaqqdfifysnvedwgsngfhdvcqpnkeldewcdrvckSidmvssn 300

Qy     301 GFHRELCPSGKGQKTCKNKLFPNSQPMAERQDMCFSCPEDQEPTMASITILDSYSAGVFV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gfhrelcpsgkgqktckNklfpnsqpmaerqdmcfscpedqeptmasitildsysagvfv 360

Qy     361 NTQRCELKCKKHHQTCCYRRPCANRLKHCIPPCLSFSEEFVCPCVIGYWKFIHEN 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ntqrcelkckkhhqtccyrrpcanrlkhcipPclsfseefvcpcvigywkfihen 415


RESULT   2
AAW00033
ID   AAW00033 standard; protein; 415 AA.
XX
AC   AAW00033;
XX
DT   10-NOV-1997  (first entry)
XX
DE   Mouse FLT4 receptor tyrosine kinase ligand VEGF C.
XX
KW   VEGF C; FLT4; receptor tyrosine kinase; VEGFR 3; gene;
KW   vascular endothelial growth factor receptor 3; ligand;
KW   angiogenesis; wound healing; lymph vessel; therapy; diagnosis.
XX
OS   Mus musculus.
XX
RN   [1]
XX
RP   1-FEB-1997.
XX
RP   01-APR-1999;  99WO-EP02427.
XX
PR   28-JUN-1996;  96US-0671573.
PR   01-AUG-1996;  96US-0691033.
PR   15-JAN-1996;  96US-0585895.
PR   14-FEB-1996;  96US-0601132.
XX
PA   (UYBE ) UNIV HELSINKI LICENSING LTD OY.
XX
PI   Alitalo K, Joukov V;
XX
DR   WPI; 1997-145688/13.
DR   N-PSDB; AAB84277.
XX
PT   FLT4 receptor tyrosine kinase ligand and related nucleic acid  used
PT   to modulate growth of endothelial cells and for diagnosis of
PT   endothelial cell diseases
XX
PS   Claim 35; Page 121-122; 184pp; English.
XX
CC   This polypeptide sequence comprises mouse VEGF C, a novel ligand
CC   that binds specifically to the FLT4 receptor tyrosine kinase
CC   (VEGFR-3), stimulating phosphorylation of the receptor, and which
CC   modulates the growth of endothelial cells. The sequence was
CC   deduced from a cDNA clone (AAB84277) obtained from a 12 day mouse
CC   embryonal cDNA library, and shows a high degree of homology to
CC   novel, claimed human VEGF C (see AAW00033) and to avian (quail)
CC   VEGF C (see AAW00044). Recombinant mouse VEGF C polypeptides can be
CC   produced that correspond to non-human mammalian variants of VEGF C.
XX
SQ   Sequence  415 AA;


  Query Match             99.8%;  Score 2428;  DB 16;  Length 415;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-174;
  Matches  414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MHLLGFFSVACSLLAAALLPGPREAPAIVAAPESGLGFSEAEPHGCHVKAFEGKDLEEGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mhllgffsiacsllaaallpgpreapaivaapesglgfseaephgchvkafegkdleega 60

Qy      61 RSVSSVDELMSVLYPDYWKMYKCQLRKGGWQHNREQVNLNSRTKETIKFAAAHYNTEILKSID 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rsvssvdelmsvlypdywkmykcqlrkggwqhnreqvnlnsrtketikfaaahyntеilksid 120

Qy     121 EWRKTQMMPREVMDVGKEFGAATNTFKPPSVVSVYRCGGVCNSEGLQCMNTSTGYLSKT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ewrktqmmprevmdvgkefgaatntfkppsvvsvyrcggvcnsegLqcmntstgylskt 180

Qy     181 LFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAANKTCP 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lfeitvplsqgpkpvtistanhtscrcmskldvyrqvhsiirrslpatlpqcqaankTcp 240

Qy     241 TNYVWNNYMCRCLAQQDFIFYSNVEDWGSNGFHDVCQPNKELDEWCDRVCKSIDMVSSN 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 tnyvwnnymcrclaqqdfifysnvedwgsngfhdvcqpnkeldewcdrvckSidmvssn 300

Qy     301 GFHRELCPSGKGQKTCKNKLFPNSQPMAERQDMCFSCPEDQEPTMASITILDSYSAGVFV 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gfhrelcpsgkgqktckNklfpnsqpmaerqdmcfscpedqeptmasitildsysagvfv 360

Qy     361 NTQRCELKCKKHHQTCCYRRPCANRLKHCIPPCLSFSEEFVCPCVIGYWKFIHEN 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ntqrcelkckkhhqtccyrrpcanrlkhcipPclsfseefvcpcvigywkfihen 415


RESULT   3
AAW12847
ID   AAW12847 standard; protein; 419 AA.
XX
AC   AAW12847;
XX
```

```
ID   1: JAN 1998  (first entry)
XX
DE   Human foetal liver kinase A binding protein flk 1bp.
XX
KW   Foetal liver kinase 1 binding protein; human; flk 1bp;
KW   receptor tyrosine kinase; vasculogenesis; angiogenesis;
KW   wound healing; tumour; therapy; antagonist; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= sig peptide
FT   Protein         21..415
FT                   /label= Mat protein
FT                   /note= "(flk 1b)"
FT   Peptide         21..65
FT                   /label= N terminal
FT                   /note= "(claim 9)"
XX
PN   WO9717442-A1.
XX
PD   15-MAY 1997.
XX
PF   05-NOV 1996;   96WO-US17584.
XX
PR   06-NOV 1995;   95US-0554374.
XX
PA   (IMMU ) IMMUNEX CORP.
XX
PI   Lyman SD;
XX
DR   WPI; 1997-296141/25.
DR   N-PSDB; AAI68811.
XX
PT   DNA encoding a human foetal liver kinase 1 binding protein -  used
PT   to treat conditions with insufficient protein, deliver diagnostic
PT   cells and identify antagonists to treat protein mediated conditions
XX
PS   Claim 1; Page 90; 92pp; English.
XX
CC   This polypeptide comprises a human foetal liver kinase 1 binding
CC   protein (flk 1bp) (see AAW17887) that binds to the receptor tyrosine
CC   kinase flk-1 expressed on vascular endothelial and other cells.
CC   The mature flk1 bp can be secreted from host cells transformed with
CC   an expression vector including an isolated flk-1bp cDNA (see SEQ ID
CC   AAI68811). Flk-1bp can be used to isolate cells to which it binds,
CC   for use in studying the roles of such cells and of flk 1 in
CC   vasculogenesis and angiogenesis. Angiogenesis inhibitors, or
CC   increased vascularisation may be clinically desirable (e.g. to
CC   suppress solid tumour growth or in wound healing, respectively).
CC   The flk-1bp can be administered to treat conditions with defective
CC   or insufficient flk 1. Polypeptides may also act as carriers to
CC   deliver diagnostic/therapeutic agents to cells which bind to it
CC   binds, to generate antibodies, and to identify flk-1bp antagonists
CC   useful for treating flk-1bp mediated conditions.
XX
SQ   Sequence  415 AA;


  Query Match             87.8%;  Score 2048;  DB 10;  Length 415;
  Best Local Similarity   85.4%;  Pred. No. 7.2e-151;
  Matches  458;  Conservative   24;  Mismatches   29;  Indels    1;  Gaps    1;

Qy       1 MHLQVLVLAALCLLTAASLYSLFSTQLSDLETEVMAYSLNLRECRLQDTGLDSEEGFIAVDAFEMPKIDDLQSPEELQCELGRPSKGHLWLKGWEPGWWPSPLEIQKDSDGDFQTVGGIDLRLRDPSGEIAFTSWLSIDNVAVLGAELAQDLKSERPKQLVLRRELLRKRFVELAVERCGCVSRATGPSLEGAPLGGVRLWHSLPVRSLRLSHLHKPSALLDLALLSCYVQACAQNHFRPNNHTALVEMQSLGKDLAPRTMGLQMTCPPACKRPLPGSLACGNWACPGTAEGDPDLLDFISGKPGPPGPKGLPGLRGPPGKDGYNGLPGDKGEPGAVGIPGTPGIDGPKGSRGAPGERGRPGLMGLKGHRGYPGLDGRNGEPGTAGPAGPRGPSGDRGSVGFPGVAGEIGPSGNIGFPGPKGPTGDPGKNGEKGHAGLAGARGAPGPDGNNGAQGPPGLQGVQGGKGEQGPPGPPGFQNLPYKTMIDPGQVMIEGTKGGFVCLVPIFDLAADDVRPQPFQEPTLESDSSEKDQGVDGAPGSRGHSGPQGLPGTAGLPGMKGHRGFSGLDGAKGDAGPALGPKGETGAPGENGTPGQKGERGAPGEGGFPGARGLAGPPGSPGNIGFPGPKGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPTGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPGPPSAGFDFSFLPQPPQEKAHDGGRYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCRDLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNPKDKRHVWFGESMTDGFQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMDQETGNLKKALLLQGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKTSRLPIIDVAPLDVGAPDQEFGFDVGPVCFL

Qy      61 RSVSQVHQDHKVLSVVDVEMKTQDSGDWWKFEHPSLEPVPMGELTDTLELRLYRCQSFHTAESGDLDTSNAVELTVKEILTAPDALDPENLTAEVDKIGTITPQSTQHWKETEAVETARTLRNLGRVLRNAETEFKHLITMDPGEIRTVAVRIRFRPLVNTGSEPSPRSDVFVYDITDSSDFSIASTEKKLFKLDSLNIGHHFVSVTNVTNHRYVRLTLRLRPSDEGTFNEMHNVNVVTFSCQIKWHPKEHMKHKDKTLDEELKSLVKEIETNSRNKKNELIAEFKILRQQMDPLTNCSSNVPFLCGDGRCKPDLEYLTQYSEDGDTCVFGPDGRLHKVESLTGREPDRGDLVFQSYNKVWLISEDNVPLYGLIHTTVKGGSRSISMPTCPYIPRPGLKFSIVNVGTNSIQMTWHLPSLTFTNGDICLQFELRMSTEEKPEEMRIIRGQPDSTHKRIGKLQPNSEYCFKVVPSRLERTGGEWSVLNITTLTAVPPSTFLQIWCIRTAYSSMNVQCSLQLDYRIKEYGEDAHLVSIRTPSFDKTVRIDNLLPGRKYVARVRMITPLGYGPFTDEDVLHLEF

Db     121 SIDNEWIKEIQHVMEDIVTENGTQLVALGKNSESFRMPEERDKAKDVLQKEMNVLRKKRNSLDNNVAHSLIATLKSKEGDLAKGAEERQAVLGQMTKILHEKSEMAEMDRNMQDIKTHLKQYVEQLYKSLKSEVQRQMKEIEKTIALKMELPEELRGLVPAGSSSRMVQLMQQQSNFLHVPFNLEMELMAPKSSVSSTSPLLDRMETDLDSFANNTTSSLSPFPSFHTVGYPNGHVTQVSGFSVSTVDSSSFISNTHPSEQGLSAYVTMQYPVQNQSEFLRDHSAESRDLGLGTEYEKMAYTGISHSDFMGTGSAYSMSTKFNQEENKTYPPQHESYSQHLSSYNDSGFLGRNSVSQDGSVTLDSSKFDPVVAMASGPGIQVFKIATPIDFSCGSIHRSATIGSIDHEEESSFRLTASEERQVDGDTSYFGAKVDEGPLQGVLIIGGVTAVFVATNGLLVLTRYLKRRKKIDPCCDVYVSNDINLTEDENEFLSQDQPKPLEDFVGLENNEIENYDDKFKLTESTIIEDPGYESDEEGIALGMVGLGDSPELQPLDEYLGADGIFTWTYDPLEGSEVDPNAPQDKPEDWDKPAKISDPKYKGTWTAPKIPNPEYFFEDLDSFPPGSGTKTFKKVIFPSLRLGGSGLKGEGLELKSEVQPKSTPQWNHVYAITGSGSLTLTGQRATAEMSKKTMKITIHEGGRAKLVSEDGAPMLRAGDYMQCVSETESGSLDSPVTCEPMEKYVFRVQGGNLALVLEPDYNMEKQYRFDLKEKNMGPVIHHFHYVSLGQQNSSKLYLDSAAFSGWKLIPDPEQNMQPVLILRDQGTDEVYMDNIGLVGTEPPNFSGFQLELQTSVVEPGVLLGTTNRSFIQVEVPDVDFNVIQTMFLRVRSISILRQEVSEPLVVLEKQGDNQSPWAYTLQQDSDVVFTAVDLFGRSLASNKVHFYFRFVNDTIPYSRVLCGNCSGRAEEDCQELQSKVHHTKCKFAFFGDRGDGNWKMLEGGCQNGSCWDYGHFTDMTFCDCRSGSNGRKCIEVEKKIFNIEELNYGAVLPPFYRPLNFTLFKDELKVITLPYNCLEGQVSNPMGLISFTIKPYSFMSVRVKGVTVSMVSSPFEENEFRPGESVNTLVGQCGNYMNHRKRRAFLDEQKLLSEDMYDGLNQSAVSVVMVDKDEFEHQVLPVTFSLQKSNSHPVSQWHNDFGTKKNRLTANQRKTEIGHTLNYGIVMFDEVHSLHLSRGSISTRLANLRSQVTFNEIEVKTNLDYGVSVIDWEDRTFIYVKDQDVCSVIQENCSQPQSSGRIMLWETVIPLRKLEVFKGPDEAGFTSPPHSQRGYVMDVVFLHTNMESGTVMITPRNQSSTPRHYEVMMYVSQDPTVPLQEPQNVQMTFLQLISNTMKVSWLPPPSIPDQAYLSEIGLFTPHLEPNGDMRHLDIFVLNTSIHSGEVEITLTRENTCAQSPVKSHKPKVMKRDVIFSENNYETLQTTDVDPGYSYDDESLEIEFEILPKPVTPNPSNPKFLVLQDVLNETVLFSWQPPHIPRKAFDGYLLMFQLVKGDILEEHVVPDAQSYTFDRLDPGIAYSFRVAAYTSIGDGAYSDLPEFIYVTDAIIPSEPPQLMLKSVNSSNAKLSWDPPSKLNGNLTGYRIIYSPNHTEDMMELDVGKDVSSFTLKDLKPDTEYIFKIQAFNGAGSGPYSEVSVKTPKGVPSSPPKDFQVSEITSTSVKLIWKPLTAKEQNGIITHFQIKRSTRSAMGEQDCLSFNGPFTNHTVGDLKPFTEYVFRIAAFTIAGIGDGPPSEPIVAKTDEAAPDMLYPVDDFQITHVMVNFAFKDPRLEHGSLLKLSYKLQTKDSWITIFSGKEIRYEHTVKDLEPDTLYEVQVSLRLKDMEGVDLTPPSAGVVTLEAVPPVNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNLQGWSQEVLEDCGSQKYNKNSARTSSFTVQDLKPFTEYVFRIVALNQMGRSPPSQPSEPVSTPEGVPSAPRLEAKAISSTEIELAWKPPEYDGGPIDGYIVEKCKKGTEVWTEVNNTPIKGTSFKVTGLIEGATYNFRVIAVNEVGESLPSEESEAVTMGEEQRPLFDKSVTVSLGDTAVFVCRVAGSPMPSISWLKNGLPLKESRHIKVLPSGSLLIQNVTKSDAGKYTCIATNSIGTDSKSAELTVQVPPSIADEPKDMEVTAGNTVNLTCQATGSPEPVVSWIFPDMDGFTIRNPQVDESGEISTSILNISSVELGDAGEYICKAVNSLGTATREFKLIVEEKPAFKKEPESLYVHENKTAVFKCEVSSSQQPSIQWLNGHVPLKSSRFSNIQVLPLGDLQISKTEESDQGKYLCVVRNSAGEDEKSFNLTVHGVPDKPTNLDFTVKSSSSVSLAWRPPADTGGRQDVTYNVICKKCGAGRPSDQHCEDCVHNTQFLPRQQGLVRQSFYHNSSCFIQCQAHNKHGPGLSSPTCKIQIPVREQITVTENSTMLIILGNLVCLALTYVFCCFRNQLKQKHPADPNKGGLGREMKDNLVPFSSSEIQTKLNHVEQMVSDRNNTQLEKEIKDLWQKFDIAHKPVVMWPSEIDLVVEKNHSLMQQDKDGFSARVGFKMNKLLNTTCNGNSLSILPDCDSKTPMGMAHGSPLGVLFFRRYRSKIMNVDLRKGVNSNYHPSEAVEKVGIMLDCDKNNLYFIEVNGASALDSEQCLFHKIVNDMIRYAEDNGHLRSPNEEESIENFIQLNVGSLDSGNHDYWLDLFPLAERFRLAKFLRDKWVKPDNVFFILDVNTQAVGVIFDCVFANGGVVQNGQSHRPSEDTIKIIMGINFCSKKDLKAGRNKAGTIGAEDPGFPTFIRELSIELVSSLSPTMVSNSHRSQSDQKVIPNSIDQAPHWAPPEYLNKFSIKSANTELKLGKGPLDEVGIYEAVYATVQDPREISWKFVDTTGKNTSVYMPTDSLIPEGKSLYVGLFDYVESGPEEISFKKGERIQNVEKVDEGWMYGTVERTKQRGDFPASYVKPSNFDPIEDMEHSEIDSRDSIISKLEVLFQGPLGSPEFMYKASKEDHIHLSHQTTVSDTSEEELNVIEKYTSEIEKAFSPFEVCGMAVGDQSCELYDIAPLDPDDSSIEDAACEVSWSTFNVDDLDVDSVELLDTDDVAGQALQNHSSWRTEGAEFSCQDPGMVLHGLQTQSLKIIDTLSSVASFCLVIVILSVMGCHSVRIQVQKHCNKSSSLQRGPPVKLVSGSKTSCMMLISMPVHSPLDHLRQTEEDSVDSEWSLGRLQVTCDPKIAAGECGAVFKAKMRDGMNCTVAVKALKGDTGPQYRSEFQQEASIMAEFDHPNIVRLIGVCKAEALMLVMEMAGGGPLHKFLVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLLVNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINFRKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKRMECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLASKVEGPPGSTQKAEAACA

RESULT   4
AAW00942
ID   AAW00942 standard; Protein; 415 AA.
XX
AC   AAW00942;
XX
DT   15-NOV 1997  (first entry)
XX
DE   Human Flt4 receptor tyrosine kinase ligand VEGF-C.
XX
KW   VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; human;
KW   vascular endothelial growth factor receptor-3; ligand;
KW   angiogenesis; wound healing; lymph vessel; lymphangioma;
KW   cancer; metastasis; therapy; diagnosis; antibody; inhibitor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..102
FT                   /label= Prepro peptide
FT   Peptide         52..227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 15)"
FT   Peptide         103..217
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 12)"
FT   Peptide         103..225
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 13)"
FT   Peptide         103..227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 14)"
FT   Peptide         113..213
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 10)"
FT   Peptide         113..227
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 11)"
FT   Peptide         131..211
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 9)"
FT   Peptide         161..221
FT                   /note= "preferred active fragment of VEGF-C,
FT                   retaining Flt4 ligand activity (Claim 8)"
XX
PN   WO9706250-A2.
XX
PD   13-FEB 1997.
XX
PF   01-AUG 1996;   96WO-FI00427.
XX
PR   28-JUN 1996;   96US-0671373.
PR   01-AUG 1995;   95US-0510144.
```

```
PP   17-JAN-1996;   96US-08585695.
PP   11-FEB-1995;   95US-00387142.
XX
PA   (UYBE ) UNIV HELSINKI LICENSING LTD OY.
XX
PI   Alitalo K,  Joukov V;
XX
DR   WPI; 1997-145008/13.
DR   N-PSDB; AAI84276.
XX
PT   Flt4 receptor tyrosine kinase ligand and related nucleic acid   used
PT   to modulate growth of endothelial cells and for diagnosis of
PT   endothelial cell diseases
XX
PS   Claim 7; Page 112-113; 189pp; English.
XX
CC   This polypeptide comprises the pre pro sequence of human VEGF-C,
CC   a novel ligand that binds specifically to human Flt4 receptor
CC   tyrosine kinase (VEGFR-3), stimulating phosphorylation of the
CC   receptor.  Its sequence was deduced from a cDNA clone (AA184276)
CC   obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL 1435)
CC   library.  The polypeptide, or its active fragments, can be
CC   expressed in transformed or transfected host cells for use in
CC   claimed methods for detecting endothelial cells (e.g. to locate
CC   lymphatic vessels, endothelial venules, Flt4 receptor in
CC   histochemical tissue) and also to modulate the growth of mammalian
CC   endothelial cells (e.g. to accelerate angiogenesis and to promote
CC   endothelial function of lymphatic vessels).  Inhibitors of
CC   VEGF-C, such as antibodies, can be used to control endothelial
CC   cell proliferation, e.g. lymphangioma or metastatic cancer.
CC   Mouse and quail VEGF-C sequences (see AAW00964.4) have also been
CC   isolated.
XX
SQ   Sequence   419 AA;


  Query Match             87.8%;  Score 2048;  DB 18;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-151;
  Matches  458;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFFLSLACSLLAAALLPGPREAPAIVAAFESGLDLSDAEPDAGEAVKAFLQKDFIPEEV 60
           |||| | |:|||||||||||:| ||||||  |||||||  |:|||| ||  |:  |||||||
Db       1 mhllgttlvacslllaaallpspregpeaaaafesglnlsdaepdagevtayaskdeiepl 60

Qy      61 KSVSSVDELMSVLYPDYIKMKVKLCGKCQWQ    QFTLNTRTGDSVKPAAAHYNLTLLK 116
           ||||||||||:||||:|||||||||||||||    |  ||:||  :::|||||||:|:|| 
Db      61 rsvssvdelmtvlypeyikmkvkscgkcqwqr   qpftlntrtgdsvkpaaahyntllk 120

Qy     117 SIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTGY 176
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||| |
Db     121 sidnewrktqcmprevcidvgkefgaatntffkppcvsvyrcggccnsegLqcmntstgy 180

Qy     177 LSKTLFEITVPLSLGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 236
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     181 lskTlfeitvplslgpkpvtistanhtscrcmskldvyrqvhsiirrslpatlpqcqaan 240

Qy     237 KTCPTNYVWNNYMCRCVAQQHTIFYSNVEDHGTENGFHEVCGPNKELDEETCQCVCKSGLR 296
           ||||||:|||:|||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     241 ktcptnymwnnhmcrcvaqehtifysnvedhgtengfhevcgpnkeldeetcqcvckSGLR 300

Qy     297 PSSCGPHKELDRNSCQCVCKNKLFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC 356
           |:|||||||||||:|||||||| |||||||||||||||||||||||||||||||||||||| 
Db     301 psscgphkeldrnscqcvckkllpsqcgaNrefdentcqcvckrtcprnqplnpgkcac 360

Qy     357 ECTESPQKCLLKGKKFHHQTCSCYRRPCANRLKHCGFCNERRCPGESSDFVCPEDKPSTDS 416
           |||| ||| ||||||||||||||||| || | |:|| |:|||||||||||||| ::
Db     361 ecteSpqkcllkgkkfhhqtcscyrrpcanrlkhcgfcnerrcpgessdfvcpedkpstds 419


RESULT   5
AAW75740
ID   AAW75740 standard; Protein; 419 AA.
XX
AC   AAW75740;
XX
DT   26-NOV-1998  (first entry)
XX
DE   Human vascular endothelial growth factor C protein.
XX
KW   Flt4; vascular endothelial growth factor C; vascular endothelial cell;
KW   lymphatic endothelial cell; myelopoiesis; angiopoiesis; inflammation;
KW   lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS   Homo sapiens.
XX
PN   WO9833917-A1.
XX
PD   06-AUG-1998.
XX
PF   02-FEB-1998;   98WO-US001975.
XX
PR   05-FEB-1997;   97US-0037540.
XX
PA   (LUBW ) LUDWIG INST CANCER RES.
PA   (UYBE ) UNIV HELSINKI LICENSING LTD.
XX
PI   Alitalo K,  Joukov V;
XX
DR   WPI; 1998-447017/38.
DR   N-PSDB; AAV75740.
XX
PT   New isolated vascular endothelial growth factor polypeptide(s)
PT   used to develop products for treating, e.g. cancers, inflammation,
PT   oedema, granulocytopenia or for wound healing or tissue
PT   transplantation
XX
PS   Claim 1; Page 112-115; 177pp; English.
XX
CC   The vascular endothelial growth factor C (VEGF C) polypeptides have
CC   activities affecting growth and migration of vascular endothelial cells,
CC   promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC   increasing vascular permeability, and affecting myelopoiesis.  The
CC   product's can be used for stimulating angiogenesses, for inhibiting
CC   anti-genesis, for stimulating lymphangiogenesis, treatment or prevention
CC   of inflammation, oedema, elephantiasis, or Milroy's disease.  They can
CC   also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC   They can also be used for modulating the growth of endothelial cells.
CC   They can also be used to stimulate lymphocyte production and maturation,
CC   and to promote or inhibit trafficking of leucocytes between tissues and
CC   lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ   Sequence   419 AA;


  Query Match             87.8%;  Score 2048;  DB 19;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-151;
  Matches  458;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

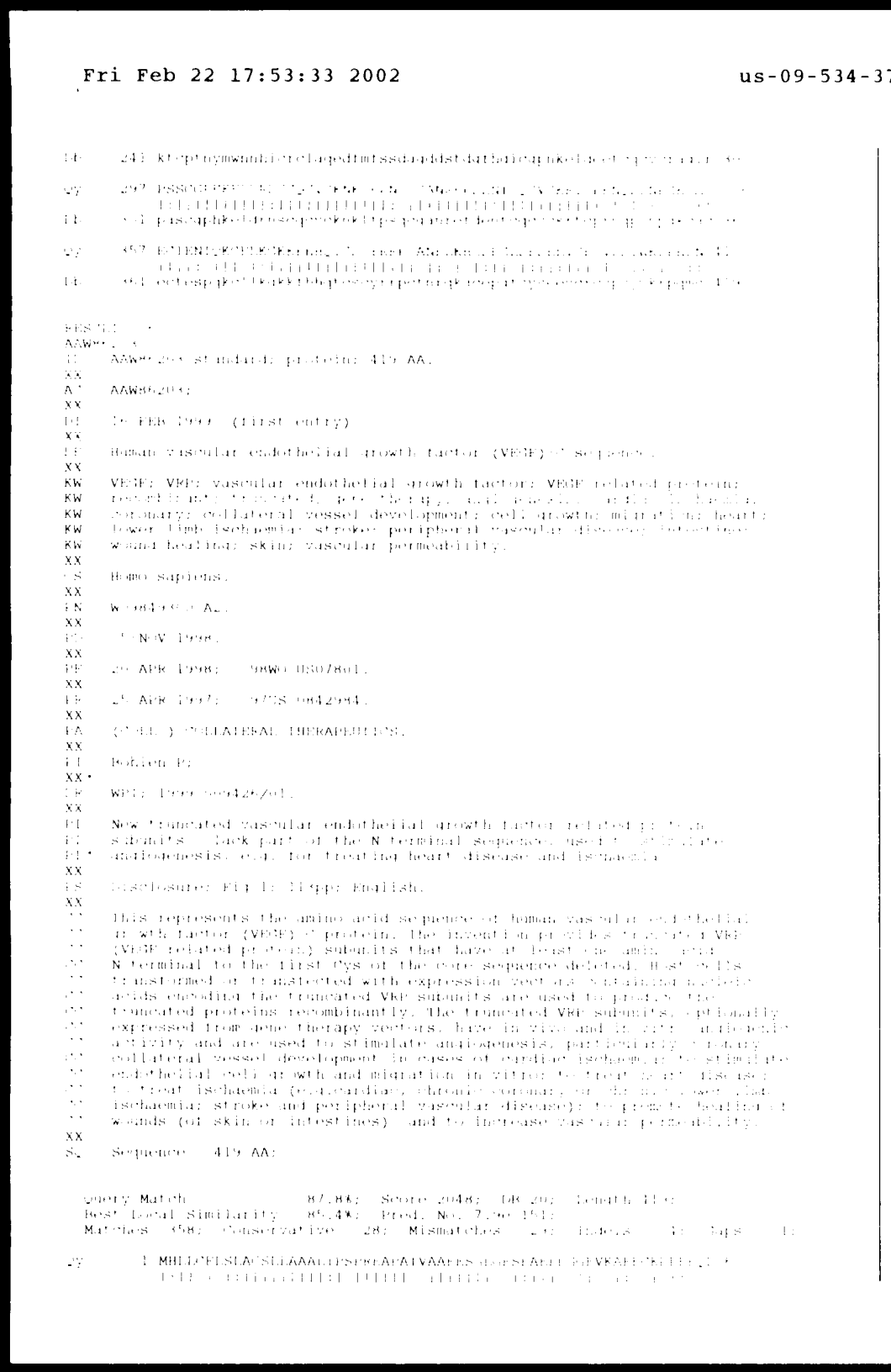
Qy       1 MHLLGFFLSLACSLLAAALLPGPREAPAIVAAFESGLDLSEAEPDAGEVKAFLQKDFIPEEV 60
           |||| | |:|||||||||||:| ||||||  |||||||  |:|||| ||  |:  |||||||
Db       1 mhllgttlvacslllaaallpspregpeaaaafesglnlsdaepdagevtayaskdeiepl 60

Qy      61 KSVSSVDELMSVLYPDYIKMKVKLCGKCQWQ    QFTLNTRTGDSVKPAAAHYNLTLLK 116
           ||||||||||:||||:|||||||||||||||    |  ||:||  :::|||||||:|:|| 
Db      61 rsvssvdelmtvlypeyikmkvkscgkcqwqr   qpftlntrtgdsvkpaaahyntllk 120

Qy     117 SIDNEWRKTQCMPREVCIDVGKEFGAATNTFFKPPCVSVYRCGGCCNSEGLQCMNTSTGY 176
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||| |
Db     121 sidnewrktqcmprevcidvgkefgaatntffkppcvsvyrcggccnsegLqcmntstgy 180

Qy     177 LSKTLFEITVPLSLGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 236
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     181 lskTlfeitvplslgpkpvtistanhtscrcmskldvyrqvhsiirrslpatlpqcqaan 240

Qy     237 KTCPTNYVWNNYMCRCVAQQHTIFYSNVEDHGTENGFHEVCGPNKELDEETCQCVCKSGLR 296
           ||||||:|||:|||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     241 ktcptnymwnnhmcrcvaqehtifysnvedhgtengfhevcgpnkeldeetcqcvckSGLR 300
```



RESULT 7
AAB10948
ID AAB10948 standard; Protein; 419 AA.
XX
AC AAB10948;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; VEGF.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30505.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164151.
XX
PA (JANS-) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel J-J, Vos JP, Dijkmans IJH, Kostelowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-412666/38.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds.
XX
PS Disclosure; Fig 11; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Ib) which has
CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vasculature

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CC   regulator.  An anti-sense molecule of the invention is useful for treating
CC   or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC   retinopathy by inhibiting angiogenic activity or inappropriate
CC   vascularization including formation and proliferation of new blood
CC   vessels, growth and development of tissues, tissue repair in a subject
CC   and tissue repair in a subject. The products of the invention are useful
CC   for preparing medicaments for treating wounds such as dermal ulcers,
CC   pressure sores, venous sores, diabetic ulcers and burns and to promote
CC   skin graft growth, tissue repair, proliferation of new blood vessels,
CC   tissue regeneration and organ repair by promoting angiogenic activity or
CC   vascularization. This sequence represents the human VEGF protein used
CC   to illustrate the method of the invention.
XX
SQ   Sequence  419 AA;


  Query Match             87.9%;  Score 2048;  DB 21;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.5e-151;
  Matches  358;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFFSVACSLLAAALLPGPREAPAIVAAELEIDLRIQERAGVNTEVKARLGKGHVEEQL 60
           ||||.|.|||||||||||.|| ||||||  |||||||  |.|||| ||  |  | | | |
Db       1 mhllattsvacslleaallpgpreapaiaaaeleidlrieeragvntevkarlgkghveeql 60

Qy      61 KGVSMSVIEPHLKAVLVPWKMYFKNQLRKGAWQ    QPETLNLRLDLKVEPAAAHYNTLTSK 116
           |||||||||.|||.|||||||||||||||||||    | ||||.|:|||||||||||||||
Db      61 ggvssvsdeimtvlypeywkmykpklrkgawqhtepnlnlrldlkveptaahynslttsk 120

Qy     117 EDDNEWRKTQVMPREVVDIGKEFGVAATNTFFKPPVVSVYHCPGGCNSESLQCMNTCEGY 176
           |||.|||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db     121 edenewrktqvmprevvdigkefgvaatntffkppvvsvyhcpggcnsesleqcmntceay 180

Qy     177 LSKELFEDIVPLSLQLPKEVVDLSFANDLSMDERPDLWSKLEVVQLVHSLIRPSLPAALLQL 236
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lskelfedivplslqlpkevvdlsfandlsmderpdlwsklevvqlvhslirpslpaallql 240

Qy     237 KLCPLNYVWNNYMCRCLAQQDFLFYSNVEDWGTGIGFPDWVGPNKELDEDLCQCVCKSGLR 296
           ||||||||||||||||||||||| ||  |||||||||||||||||||||||||||||||||
Db     241 klcplnyvwnnymcrclaqqdflfysnvedwgtgigfpdwvgpnkeldedlcqcvcksglr 300

Qy     297 PSSCGPHKELDRNSCQCVCKNKLFPNPQCANRGFSFNEKVVKCAPQLPNAVKYVSTHKSLW 356
           |:|||||||||.|||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 psscgphkeldrnscqcvcknklfpnpqcanrgfsfnekvvkcapqlpnavkyvsthksLw 360

Qy     357 HYLENLQKCELKSKEHHQLYCSYKMPFCANEGKFFHQWRWIRIDTSHLSKYRIKFVCEHQL 416
           |||| ||| |||||||||||||||||| || | ||| |||||||||||||||||||| ||
Db     361 hylenlqkcelkskehhqlycsykmpfcanegkffhqwrwiridtshlskyrikfvcehql 420


RESULT  8
AAB72048
ID   AAB72048 standard; protein; 419 AA.
XX
AC   AAB72048;
XX
DT   31-JAN-2001  (first entry)
XX
DE   Human VEGF-C protein sequence.
XX
KW   Human; EIA4; tmc-like tyrosine kinase 4; lymphoedema;
KW   vascular endothelial growth factor receptor 3; VEGFR-3;
KW   Milroy Nonne syndrome; lymphoedema praecox; VEGF-C;
KW   vascular endothelial growth factor C.
XX
OS   Homo sapiens.
XX
PN   WO200058511-A1.
XX
PD   05-OCT-2000.
XX
PF   29-MAR-1999;  99WO-US006133.
XX
PR   26-MAR-1999;  99WO-US006133.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Partanen KE, Alitalo K, Pajusola K, Karkkainen M;
XX
DR   WPI; 2000-679208/66.
DR   N-PSDB; AAZ62406.
XX
PT   Screening a human subject for increased risk of developing a lymphatic
PT   disorder, comprises assaying a nucleic acid to determine a mutation
PT   affecting the sequence of a vascular endothelial growth factor
PT   receptor 3
XX
PS   Disclosure; Page 60-61; 76pp; English.
XX
CC   The present sequence is the protein sequence for the human vascular
CC   endothelial growth factor C (VEGF-C). It was used to demonstrate the
CC   methods of the invention, which involve the screening of individuals to
CC   determine which vascular endothelial growth factor receptor 3 (VEGFR-3,
CC   also known as FLT4 or tmc like tyrosine kinase 4) alleles they possess
CC   and thus their likelihood of developing hereditary lymphoedema.
CC   Conditions associated with lymphoedema include Milroy Nonne syndrome,
CC   which is early onset lymphoedema and lymphoedema praecox, which is late
CC   onset
XX
SQ   Sequence  419 AA;


  Query Match             87.9%;  Score 2048;  DB 21;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.5e-151;
  Matches  358;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFFSVACSLLAAALLPGPREAPAIVAAELEIDLRIQERAGVNTEVKARLGKGHVEEQL 60
           ||||.|.|||||||||||.|| ||||||  |||||||  |.|||| ||  |  | | | |
Db       1 mhllattsvacslleaallpgpreapaiaaaeleidlrieeragvntevkarlgkghveeql 60

Qy      61 KGVSMSVIEPHLKAVLVPWKMYFKNQLRKGAWQ    QPETLNLRLDLKVEPAAAHYNTLTSK 116
           |||||||||.|||.|||||||||||||||||||    | ||||.|:|||||||||||||||
Db      61 ggvssvsdeimtvlypeywkmykpklrkgawqhtepnlnlrldlkveptaahynslttsk 120

Qy     117 EDDNEWRKTQVMPREVVDIGKEFGVAATNTFFKPPVVSVYHCPGGCNSESLQCMNTCEGY 176
           |||.|||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db     121 edenewrktqvmprevvdigkefgvaatntffkppvvsvyhcpggcnsesleqcmntceay 180

Qy     177 LSKELFEDIVPLSLQLPKEVVDLSFANDLSMDERPDLWSKLEVVQLVHSLIRPSLPAALLQL 236
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 lskelfedivplslqlpkevvdlsfandlsmderpdlwsklevvqlvhslirpslpaallql 240

Qy     237 KLCPLNYVWNNYMCRCLAQQDFLFYSNVEDWGTGIGFPDWVGPNKELDEDLCQCVCKSGLR 296
           ||||||||||||||||||||||| ||  |||||||||||||||||||||||||||||||||
Db     241 klcplnyvwnnymcrclaqqdflfysnvedwgtgigfpdwvgpnkeldedlcqcvcksglr 300

Qy     297 PSSCGPHKELDRNSCQCVCKNKLFPNPQCANRGFSFNEKVVKCAPQLPNAVKYVSTHKSLW 356
           |:|||||||||.|||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 psscgphkeldrnscqcvcknklfpnpqcanrgfsfnekvvkcapqlpnavkyvsthksLw 360

Qy     357 HYLENLQKCELKSKEHHQLYCSYKMPFCANEGKFFHQWRWIRIDTSHLSKYRIKFVCEHQL 416
           |||| ||| |||||||||||||||||| || | ||| |||||||||||||||||||| ||
Db     361 hylenlqkcelkskehhqlycsykmpfcanegkffhqwrwiridtshlskyrikfvcehql 420


RESULT  9
AAY76749
ID   AAY76749 standard; protein; 419 AA.
XX
AC   AAY76749;
XX
DT   17-AUG-2000  (first entry)
XX
DE   Human preprovascular endothelial growth factor C.
XX
```

KW Human; receptor tyrosine kinase; RTK; Flt4; tms like tyrosine kinase 4;
KW VEGFR-3; vascular endothelial growth factor receptor 3; chromosome 5q35;
KW cytostatic; tumour imaging; anti tumour therapy; treatment; diagnosis;
KW neoplastic disease; lymphoma; carcinoma; breast; sputum; cancer;
KW sarcoma; melanoma; VEGF-C; vascular endothelial growth factor C.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= Signal_peptide
FT Peptide 32..103
FT /label= N-terminal_peptide
FT /note= "cleavage of this peptide from partially processed
FT VEGF-C produces a fully processed mature form that
FT of 21-23 kD which has high affinity to VEGFR-2"
FT Protein 104..227
FT /label= Mature_VEGF-C
FT Peptide 228..419
FT /label= C-terminal_peptide
FT /note= "Has a pattern of spaced cysteine residues
FT reminiscent of a Balbiani ring 1 protein (BR1) sequence;
FT cleavage of signal peptide and the C-terminal
FT peptide produces a partially processed form of VEGF-C
FT about 29 kD which has high affinity to Flt1 (VEGFR-1)"
FT Binding site 114..218
FT /note= "Binds and stimulates VEGFR-3 tyrosine kinase;
FT at position 156 is essential for VEGFR-2 binding and at
FT 165 is essential for VEGFR-2 and VEGFR-3 binding"
FT Region 141..211
FT /note= "important for VEGFR-3 activity"
XX
PN WO 00/27994-A1
XX
PD 18-MAY-2000
XX
PF 09-NOV-1999; 99WO-US26525.
XX
PR 09-NOV-1998; 98US-0107679.
XX
PA (LIWA-) LUDWIG INST CANCER RES.
PA (HELS-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Kaipainen A, Vaitkus K, Jussila L;
XX
DR WPI; 2000-317850/27.
XX
PT Treating neoplastic diseases such as lymphoma, carcinoma, breast and
PT and sarcomas, involves administering a compound capable of inhibiting
PT binding of ligand proteins to tms-like tyrosine kinase 4 receptor
XX
PS Example 15.1; Page 140-142; 118pp; English.
XX
CC The patent discloses a method to treat neoplastic disease characterised
CC by expression of the tms like tyrosine kinase 4 (Flt4) receptor. Flt4
CC referred as vascular endothelial growth factor receptor-3 (VEGFR-3) is
CC endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC method involves administering a compound that inhibits binding of a
CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC endothelial cells. The compound is useful for treating neoplastic disease
CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
CC for manufacturing medicament useful for diagnostic screening, prognosis and
CC treatment of malignancies characterised by Flt4 expressing cells.
CC The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb
CC and 4.5 kb mRNAs which differ in their 3' sequences and are
CC differentially expressed in HEL and DAMI cell lines. Flt4
CC belongs to a subfamily of class III receptor tyrosine kinases (RTKs).
CC It is used as a target for tumour imaging and anti-cancer therapy.
CC The present sequence is a human prepro vascular endothelial growth
CC factor C (VEGF-C), a specific example of Flt4 binding compound.
XX
SQ Sequence 419 AA;

Query Match 87.8%; Score 2048; DB 21; Length 419;
Best Local Similarity 85.4%; Pred. No. 7.9e-151;
Matches 358; Conservative 28; Mismatches 29; Gaps 4; Indels 1;

Qy 1 MHLLGFFSVACSLLAAALLPGPREAPAIVAAPESGLDLFSEAEPEQGFVKAFEGKDLEFEQL 60
Db 1 MHLLGFLSLACSLLAAALLPSPREAPAIVAAPESGLDLFSEAEPEQGFVKAFEGKDLEFEQL 60

Qy 61 PSVDVPSLLNEVLAIDVWERMVVPCQLPPEGDWL--SPGENPPDSLVPEFAAAHFYNLEIGK 118
Db 61 PSVSSSDLLAPGSTPPQYWKMYKHQLKPDWEYTNLRLKEKPRASQHTDTSVGLGAQAAGGLT 120

Qy 119 TLPNLWRLYSKPSANLVLVGHSLGAFLAIDTYTAVRQAPASNGDVQVTVLALLDPAWVLQEH 178
Db 121 SLDSQWRKFSPPSEKLISLYGDEFDMGALMAGLSAVKELRGFTQSRMDLSPVDLVITDRSEN 180

Qy 179 LNETLVFERSVPLSGPLEVLITANHTGFMSESDSVVRSLVRCLASKLPAPSTLSAAR 236
Db 181 LSKTTAFIRSPLSPPPEPTTISTANTSSPDMSKLDVYRPCHSTTRSIPAPGPPQAAR 240

Qy 237 RFTLTENYVNKNNYMRSLAQQCFETTQNVESKSCNCTRPAVSPGKEELSSTTQWVTKSIE 296
Db 241 KTGPGTNYMWWNHLRLQLPETMISSTAADTSTNTDLDMQAVKEDPAWKLPFPRESLALT 300

Qy 297 RSCSDHELSSL-VKERRRLNG-ANNRTTSNDSLPVKRPLNLPGNSKSVA 343
Db 301 PSPGAPLKELRDSGPQWKKLPSPGAATGDDGTGSEAGSVSPDGQEVAR 350

Qy 457 RGTENLQSLRRCSSLHGQGLSVRSSANRLRDEVHLVSQLESLSERVGELSSQVAEYRSISE 516
Db 451 RATDSPGPKSLRARRKLDGPVGYGPFCPHGGLASYSSGGGSPSWKRPPPS 499

RESULT 10
AAY70982
ID AAY70982 standard; Protein; 419 AA.
XX
AC AAY70982;
XX
DT 09-AUG-2000 (first entry)
XX
DE Human vascular endothelial growth factor (VEGF)-C protein.
XX
KW Vascular endothelial growth factor C; VEGF; human; re-endothelialisation;
KW vascular endothelial growth factor receptor; VEGFR; vascular trauma;
KW blood vessel; cardiovascular surgery; anti restenosis agent; prosthesis;
KW restenosis; stenosis; percutaneous transluminal coronary angioplasty.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= Signal_peptide
FT /note= "Cleavage results in partially processed VEGF-C
FT protein (29 KD)"
FT Peptide 32..103
FT /label= Amino_terminal_peptide
FT /note= "Cleavage results in fully processed mature
FT VEGF-C protein (21-23 KD)"
FT Protein 104..227
FT /label= Mature human VEGF-C
FT /note= "Processed vascular epithelial growth factor-C"
FT Binding site 88
FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT Active site 141..211
FT /note= "Essential for biological activity of protein"
FT Binding site 157
FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT Binding site 156
FT /note= "Essential for VEGFR-2 binding"
FT Binding site 165

```
FT                   /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT   Peptide         229..419
FT                   /label= Carboxy terminal peptide
FT                   /note= "Cleavage results in partially processed VEGF-C
FT                   protein (29 kD)"
XX
PN   WO0002912-A2.
XX
PD   13-JAN-2000.
XX
PF   26-JUN-1999;   99WO-US014054.
XX
PR   26-JUN-1998;   98US-0090867.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD OY.
PA   (YLAH/) YLA HERTTUALA S.
XX
PI   Yla herttuala S, Alitalo K, Hiltunen MO, Heinsch MM, Achen MG;
XX
DR   WPI; 2000-130484/10.
DR   N-PSDB; AAB00455, AAB00456.
XX
PT   Preventing stenosis and restenosis in mammals using vascular
PT   endothelial growth factor proteins or the nucleic acids encoding them
XX
PS   Claim 5; Page 51-53; 61pp; English.
XX
CC   The present amino acid sequence is the complete human prepro-vascular
CC   endothelial growth factor (VEGF) C. VEGF-C has the ability to stimulate
CC   re-endothelialisation of an injured blood vessel, without significant
CC   stimulation of smooth muscle cell proliferation. It can bind to and
CC   stimulate VEGFR-2 (vascular endothelial growth factor receptor-2) and/or
CC   VEGFR-3 phosphorylation in cells that express such receptors. An
CC   anti-restenosis agent comprising either a VEGF-C gene or protein is
CC   used in a method to reduce or prevent restenosis and stenosis of a blood
CC   vessel following vascular trauma (e.g., cardiovascular surgery and
CC   percutaneous transluminal coronary angioplasty.
XX
SQ   Sequence  419 AA;
```

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  Query Match             87.8%;  Score 2048;  DB 2;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-151;
  Matches  458;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFFLSLACSLLAAALLPGPREAPAIVAAFESGLDLSDAEPDAGEAVKAFEGKLDIEVQ 60
           |||| | |:|||||||||||:| ||||||  ||||||  |:|||| ||  ||  ||||||
Db       1 mhlfpfisvcvllaaallpgpreapaaaafesglnlsdaepdagealyaskdleeqf 56

Qy      61 KGVSGSVDELMSVLYPDYWKMYKCQLRKGGWQ    QPELNTRYGDLVEAFAAHYNTEIIK 116
           ||||||||||:|||||||||||||||||||||    | ||:|| :::|||||||||||||
Db      57 rgvsgsvdelmtvlypeywkmykcqlrkgawhhnrepanlnsrtefikraaqayntelik 116

Qy     117 GTDNEWKEIQFMQEVCTDVSLGVRVFDMGGQRSERRKWIHCFENVNAIMFCVALSEYDQVLV 176
           |||||||:|||||||||||||||||| |||||||||||||||||||||||||||||||| |
Db     117 gtdnewkfiqfmqevctdvslgvrvfdmggqrserrkwihcfenvnaimfcvalseydqvlv 176

Qy     177 ESKTLDPEIVPLHSQGPKPVTETGFANRLTGWGSKLLVYPQVHICERPSLPAILPQVAAN 236
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     177 esktldpeivplhsqgpkpvtetgfanrltgwgsklLvypqvhicerpslpailpqvaan 236

Qy     237 KICPLNYVWNNYMFCPLADQHFIFYSNVEDHSLNGFTDDVSFNKFELLPLCVCKSSLP 296
           |||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db     237 kicplnyvwnnymfcpladqhfifysnvedhslngftddvsfnkfellplcvckssLp 296

Qy     297 DSSCGPHKELPRGCVCNKLEPNSCANPFDENKCVCKRLVPINPNNDKFDLNKDKVV 356
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     297 dssCgphkelprgcvcnklepnscanpfdenkcvckrlvpinpnndkfdlnkdkvv 356

Qy     357 PGTENLVGCELKKKPRHQLDSQYRRFCANKLKHCPDLSSFSEEVCKVCVKWKRNDN 415
           |||| ||| ||||||||||||||||||| || | |:|| |:|||||||||||||| ||
Db     357 pgtdnlvgcdlkkkprhqldsqyrrfcankLkhcpdlssfseevckvcvkwkrndn 415
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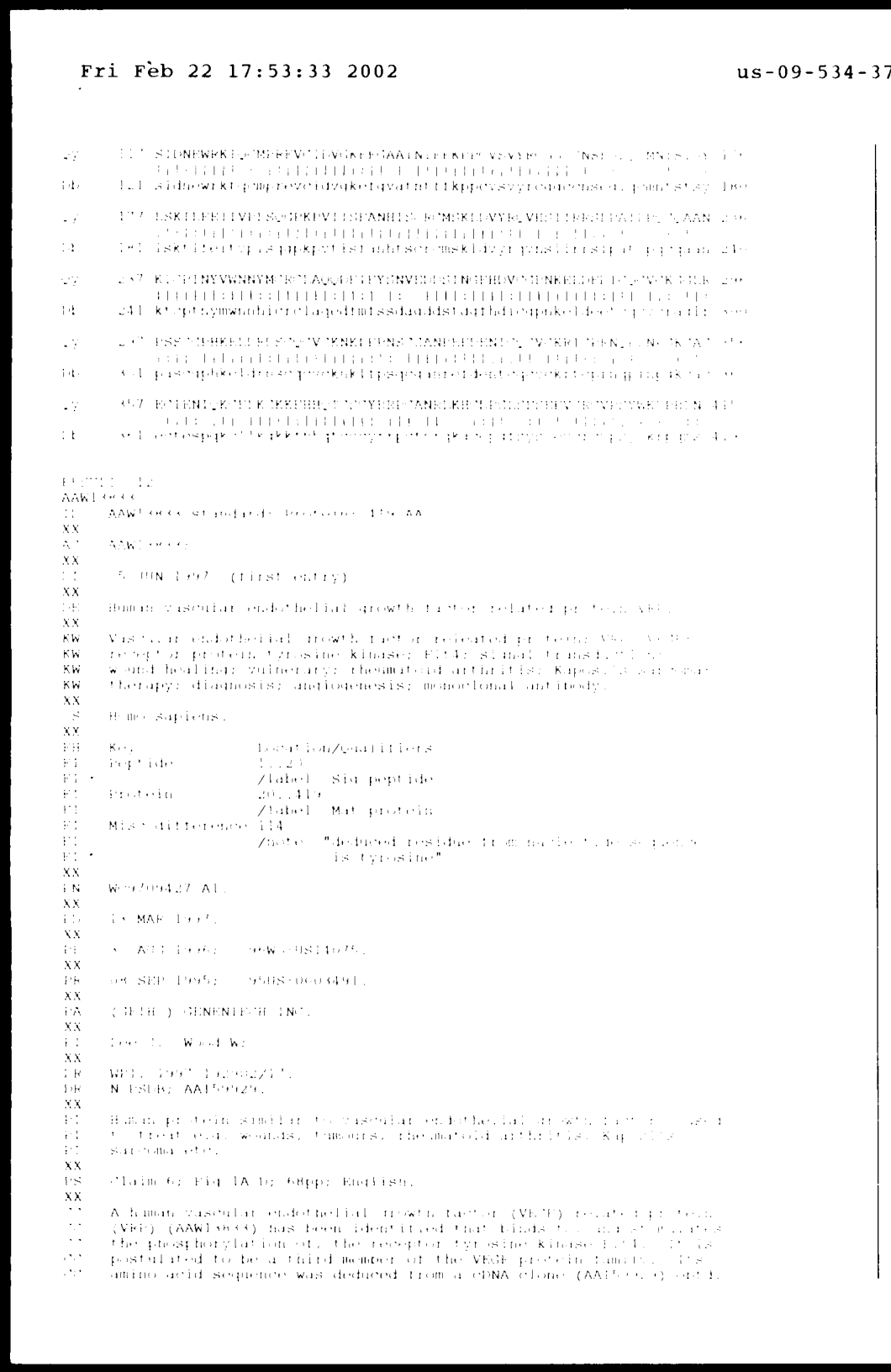
RESULT  11
AAB67605
ID   AAB67605 standard; Protein; 419 AA.
XX
AC   AAB67605;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Human VEGF-C.
XX
KW   Human; gene therapy; lymphatic disorder; hereditary lymphoedema; ss4.
KW   vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-C; VEGF-1;
KW   tyrosine kinase-4.
XX
OS   Homo sapiens.
XX
RN   [A228470-A1.
XX
RD   26-SEP-2000.
XX
RP   26-SEP-1999;   99EP-A228470.
XX
PR   26-MAR-1999;   99WO-US006183.
PR   16-AUG-1999;   99US-0375248.
XX
PA   (UYPI ) UNIV PITTSBURGH.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD OY.
PA   (LUDW ) LUDWIG INST CANCER RES.
XX
PI   Alitalo K, Ferrell RE, Finegold DN, Karkkainen M;
XX
DR   WPI; 2001-007762/02.
DR   N-PSDB; AAC68953.
XX
PT   Screening a human for an increased risk of developing lymphatic
PT   disorder comprises assaying nucleic acid for alterations in the
PT   sequences expressing vascular endothelial growth factor receptor-3
XX
PS   Disclosure; Pages 62-63; 99pp; English.
XX
CC   The present invention relates to a method for screening a human subject
CC   for an increased risk of developing a lymphatic disorder e.g. hereditary
CC   lymphoedema. The method comprises assaying nucleic acid of a human
CC   subject to determine a presence or an absence of a mutation altering the
CC   sequence or expression of vascular endothelial growth factor receptor-3
CC   (VEGFR-3)/tyrosine kinase-4 (FLT4) allele (see AAC68953 and
CC   AAB67604) and determining an increased risk of developing lymphatic
CC   disorder from presence or absence of the mutation. The presence of a
CC   mutation altering the encoded amino acid sequence or expression of at
CC   least 1 VEGFR-3 allele in the nucleic acid correlates with an increased
CC   risk of developing a lymphatic disorder. Treatment for hereditary
CC   lymphoedema can be provided through the administration of vascular
CC   endothelial growth factor-C (VEGF-C) and vascular endothelial growth
CC   factor-D VEGF-D genes (via gene therapy) and proteins. The present
CC   sequence is the protein sequence for VEGF-C.
XX
SQ   Sequence  419 AA;
```

```
  Query Match             87.8%;  Score 2048;  DB 2;  Length 419;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-151;
  Matches  458;  Conservative   28;  Mismatches   29;  Indels    4;  Gaps    1;

Qy       1 MHLLGFFLSLACSLLAAALLPGPREAPAIVAAFESGLDLSDAEPDAGEAVKAFEGKLDIEVQ 60
           |||| | |:|||||||||||:| ||||||  ||||||  |:|||| ||  ||  ||||||
Db       1 mhlfpfisvcvllaaallpgpreapaaaafesglnlsdaepdagealyaskdleeqf 56

Qy      61 KGVSGSVDELMSVLYPDYWKMYKCQLRKGGWQ    QPELNTRYGDLVEAFAAHYNTEIIK 116
           ||||||||||:|||||||||||||||||||||    | ||:|| :::|||||||||||||
Db      57 rgvsgsvdelmtvlypeywkmykcqlrkgawhhnrepanlnsrtefikraaqayntelik 116
```



RESULT 12
AAW18933
ID AAW18933 standard; Protein; 125 AA.
XX
AC AAW18933;
XX
DT 5-JUN-1997 (first entry)
XX
DE Human vascular endothelial growth factor related protein VRP.
XX
KW Vascular endothelial growth factor related protein; VRP; VEGF;
KW receptor protein tyrosine kinase; FLT4; signal transduction;
KW wound healing; vulnerary; rheumatoid arthritis; Kaposi's sarcoma;
KW therapy; diagnosis; angiogenesis; monoclonal antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig peptide
FT Protein 20..419
FT /label= Mat protein
FT Misc-difference 114
FT /note= "deduced residue from nucleic acid sequence
FT is tyrosine"
XX
PN WO9709427-A1.
XX
PD 13-MAR-1997.
XX
PF 4-SEP-1996; 96US-0026491.
XX
PR 08-SEP-1995; 95US-0003491.
XX
PA (HUMA-) GENENTECH INC.
XX
PI Lee J, Wood W;
XX
DR WPI; 1997-172022/15.
DR N-PSDB; AAI50029.
XX
PT Human protein similar to vascular endothelial growth factor -
PT treat oral wounds, tumours, rheumatoid arthritis, Kaposi's
PT sarcoma etc.
XX
PS Claim 6; Fig 1A-D; 68pp; English.
XX
CC A human vascular endothelial growth factor (VEGF) related protein
CC (VRP) (AAW18933) has been identified that binds to and induces
CC the phosphorylation of, the receptor tyrosine kinase FLT4. It is
CC postulated to be a third member of the VEGF protein family. Its
CC amino acid sequence was deduced from a cDNA clone (AAI50029) obtd.
CC from a placenta (-1) library. Recombinant VRP can be produced in
CC transformed host cells and used to promote growth of vascular and
CC lymph endothelial cells; to stimulate phosphorylation of the
CC tyrosine kinase domain of a Flt4 receptor; as a diagnostic or as an
CC additive to cell cultures; to screen for (anti)agonists; and to
CC raise monoclonal antibodies used to treat conditions associated
CC with excessive neovascularisation or vascular permeability. VRP
CC may make it possible to avoid coronary by pass surgery by
CC stimulating growth of the collateral circulation.
XX
SQ Sequence 419 AA;

Query Match 87.4%; Score 2096; DB 2; Length 419;
Best Local Similarity 86.2%; Pred. No. 4e-154;
Matches 452; Conservative 28; Mismatches 36; Indels 4; Gaps 1;

Qy 1 MHLLGFFSLACSLLAAALTFSFEMDAFAIVAAPESGLCPEGAPPAGQPVVKAFPGKELFLL 60
Db 1 MHLIATTSVACSLAAALPLPGPEDSAAAATQSQLDLSDAFPSNFPASTAYGSGDRPLL 60

Qy 61 RCVQVELELMYQLTYGFRMSVE-GQPEAGAPLGESTRRLDLLRLQLTELELELILT 119
Db 61 RCVQVELELMYQLTYGFRMSVEKGQPEAGAPLGESTRRLDLLRLQLTELELELILT 120

Qy 120 SQKRDEMWTGAKMALLVTLLVMLLIVSLGSMYLFCKQAAGPVTLGPLPPVAAVNPDA 179
Db 121 SQKRDEMWTGAKMALLVTLLVMLLIVSLGSMYLFCKQAAGPVTLGPLPPVAAVNPDA 180

Qy 180 EGLEGQLERALKVTEDDKNLVDLIDKFLGLQEVVGEVNDLLGTSQFYDLSIPIDSMPE 239
Db 181 EGLEGQLERALKVTEDDKNLVDLIDKFLGLQEVVGEVNDLLGTSQFYDLSIPIDSMPE 240

Qy 240 FDIRITETQPRSVSIIQAEMSRLQITDVSVLVSLLSLSVITGPVIHLSDVETVASDGIC 299
Db 241 FDIRITETQPRSVSIIQAEMSRLQITDVSVLVSLLSLSVITGPVIHLSDVETVASDGIC 300

Qy 300 SSIGRLMDSVGMVQPILGEYYSLNDSLLVSLVNNLGTFTLRSGSEMKISKDVQDIKLLY 359
Db 301 PSEQPHKEDERHSDPQYQKNKLTPSPIDHQEMTSDSQHSTPQFLPQENPLHVPPETES 360

Qy 360 DCTENLQKCPLKGMKEPHRQIDSGYRRPVANFLKRCDEGLSESEEVCSCVEGYWRKPPLN 419
Db 361 DCTQSPQKCPLKEMTFRSGLDEEYQEPIANPLSNLRNSVTTKHKDMVWLTVSGSSHPGS 420

RESULT 13
AAY80518
ID AAY80518 standard; Protein; 419 AA.
XX
AC AAY80518;
XX
DT 16-NOV-1999 (first entry)
XX
DE Vascular endothelial growth factor 2 (VEGF-2).
XX
KW human vascular endothelial growth factor-2; VEGF-2;
KW vascular endothelial cell growth; endothelial cell migration;
KW angiogenesis; blood pressure; blood flow; immune system disorder;
KW immune cell; cancer; autoimmune disorder; blood protein disorder;
KW ataxia telangiectasia; common variable immunodeficiency;
KW Digeorge syndrome; HIV infection; HTLV BLV infection;
KW leukocyte adhesion deficiency syndrome; lymphopenia;
KW phagocytic bacterial dysfunction; severe combined immun. deficiency;
KW Wiskott-Aldrich disorder; anemia; thrombocyt-penia; hemoglobinuria;
KW allergy; asthma; allergic asthma.
XX
OS Homo Sapiens.
XX
PN WO9946364-A1.
XX
PD 16-SEP-1999.
XX

PT 10-MAR-1999; 99WO-US005021.
XX
PR 13-MAR-1998; 98US-0042105.
PR 30-JUN-1998; 98US-0091067.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben S, Wen L, Ni J;
XX
DR WPI; 1999-551697/46.
DR N-PSDB; AAZ10523.
XX
PT New human vascular endothelial growth factor 2, used in treating
PT immune disorders and cancers
XX
PS Claim 12; Fig 1A-1J; 222pp; English.
XX
CC The present sequence represents vascular endothelial growth factor 2
CC (VEGF-2). The VEGF-2 polypeptides have activities similar to VEGF. The
CC VEGF-2 polypeptides stimulate the growth of vascular endothelial cells,
CC stimulate endothelial cell migration, stimulate angiogenesis, decrease
CC blood pressure, and increase blood flow. The polynucleotides and
CC polypeptides can be used for preventing, treating or ameliorating a
CC medical condition. The VEGF-2 polypeptides or polynucleotides may be
CC useful in treating deficiencies or disorders of the immune system, by
CC activating or inhibiting the proliferation, differentiation, or
CC mobilization (chemotaxis) of immune cells. The disorders or these immune
CC deficiencies or disorders may be genetic, somatic, such as cancer or
CC some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or
CC infections. Examples of immunologic deficiency syndromes include blood
CC protein disorders, ataxia telangiectasia, common variable
CC immunodeficiency, Digeorge syndrome, HIV infection, HIV-mediated,
CC leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte
CC bactericidal dysfunction, severe combined immunodeficiency (SCID),
CC Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.
CC They can also be used to modulate hemostatic or thrombolytic activity.
CC Similarly allergic reactions and conditions such as asthma (particularly
CC allergic asthma) or other respiratory problems, may also be treated.
XX
SQ Sequence 411 AA;

Query Match 87.4%; Score 2038; DB 20; Length 411;
Best Local Similarity 85.0%; Pred. No. 4.7e-150;
Matches 356; Conservative 29; Mismatches 30; Indels 1; Gaps 1;

Qy 1 MHLLGPLSLACSLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL 60
MH+L+P+SLA SLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL
Db 1 MHILSPFSLATSLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL 60

Qy 61 RGVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWG--QPTLNPRDEVELDSVKLEAAAHYNTSILK 118
+GVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWG QPTLNPRDEVELDSVKLEAAAHYNTSILK
Db 61 KGVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWGPQPTLNPRDEVELDSVKLEAAAHYNTSILK 120

Qy 119 SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY 176
SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY
Db 121 SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY 180

Qy 177 LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 236
LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN
Db 181 LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 240

Qy 237 KTCPTNYVWNNYMRCRLAQQGDPETYYSNVEDFSTNGEHDVCYGPNKELDEETCQCVCKSGH 296
KTCPTNYVWNNYMRCRLAQQGDPETYYSNVEDFSTNGEHDVCYGPNKELDEETCQCVCKSGH
Db 241 KTCPTNYMWNNHICRCLAQQGDPMTNSSDAQDDSTDQTDTSTAVGPQNKELDEETCQCVCKSGH 300

Qy 297 RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC 356
RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
Db 301 RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC 360

Qy 357 ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN 416
ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN
Db 361 ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN 420

RESULT 14
AAY22320
ID AAY22320 standard; Protein; 419 AA.
XX
AC AAY22320;
XX
DT 22-SEP-1999 (first entry)
XX
DE Full length human VEGF2 protein sequence.
XX
KW VEGF2; vascular endothelial growth factor 2; angiogenesis; bone damage;
KW endothelial cell proliferation; tissue damage; therapy.
XX
OS Homo sapiens.
XX
PN US5994564-A.
XX
PD 03-AUG-1999.
XX
PF 24-DEC-1997; 97US-0999811.
XX
PR 24-DEC-1997; 97US-0999811.
PR 08-MAR-1994; 94US-0207560.
PR 06-JUN-1995; 95US-0465968.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Chen L, Ruben S, Rosen CA;
XX
DR WPI; 1999-443686/37.
DR N-PSDB; AAX84837.
XX
PT Vascular endothelial growth factor 2 for wound healing and vascular
PT repair
XX
PS Claim 1; Fig 1; 49pp; English.
XX
CC This sequence is the vascular endothelial growth factor 2 (VEGF-2),
CC of the invention. The isolated polypeptide is useful for stimulating
CC angiogenesis, by promoting the proliferation of endothelial cells, for
CC the treatment of a wound, or for the treatment of tissue or bone damage.
XX
SQ Sequence 419 AA;

Query Match 87.4%; Score 2038; DB 20; Length 419;
Best Local Similarity 85.0%; Pred. No. 4.7e-150;
Matches 356; Conservative 29; Mismatches 30; Indels 1; Gaps 1;

Qy 1 MHLLGPLSLACSLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL 60
MH+L+P+SLA SLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL
Db 1 MHILSPFSLATSLLAAALLPSPREAPATVAAFESGLDFSDAEPDAGEVKAFESKDLEPQL 60

Qy 61 RGVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWG--QPTLNPRDEVELDSVKLEAAAHYNTSILK 118
+GVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWG QPTLNPRDEVELDSVKLEAAAHYNTSILK
Db 61 KGVSSVDERLMSVLEPIYWLGMKYRSQGERKGAWGPQPTLNPRDEVELDSVKLEAAAHYNTSILK 120

Qy 119 SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY 176
SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY
Db 121 SIDNEWKKTQMPREVMTIDVGSVSRNLAAINEIFKENVKFSWSVYVEKANNSFSNLEEVY 180

Qy 177 LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 236
LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN
Db 181 LSKIEFELTIVPLSQPKPVTISFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 240

Qy 237 KTCPTNYVWNNYMRCRLAQQGDPETYYSNVEDFSTNGEHDVCYGPNKELDEETCQCVCKSGH 296
KTCPTNYVWNNYMRCRLAQQGDPETYYSNVEDFSTNGEHDVCYGPNKELDEETCQCVCKSGH
Db 241 KTCPTNYMWNNHICRCLAQQGDPMTNSSDAQDDSTDQTDTSTAVGPQNKELDEETCQCVCKSGH 300

Qy 297 RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC 356
RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC
Db 301 RSRSSQHHKELDRDSCQCVCKNKLFPNSCGANREFDENTCQCVCKRTCPRNQPLNPGKCAC 360

Qy 357 ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN 416
ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN
Db 361 ECTENTQKCYQLKGKKPHIQTCSGHCPADQLKANGQGIEDFVFSETVDVGDSPDFIQCVKN 420

```
Db      561 pasqaphkeldtnsqpyqkkklfpspeqaaqrefdqahtpdyqkdfqyeggpaiqakqaf 620

Qy      477 E*IENIQKCFLKIKKFHHQLDSQYKRPKVANEIKDLSSLSERFVIDVVLQYWFEIHQLN 536
            ||| || | |||||||||| |||||| || | |||| |||| ||| |||||||||||| ||
Db      621 ewlkrtpgqdlkdkalfqehkqlesgyyfqfnaqnnegesvysvsipptegdcvtsmlty 680

RESULT  1
AAY47144
ID   AAY47144 standard; protein; 419 AA.
XX
AC   AAY47144;
XX
DT   22-DEC-2000 (first entry)
XX
DE   Vascular endothelial growth factor 2 (VEGF 2)
XX
KW   Vascular endothelial growth factor 2; VEGF 2; retinal; eye disease;
KW   treatment; injury; degeneration; photoreceptor; cyst;
KW   cotton wool spots; retinitis pigmentosa; human;
KW   age related macular degeneration; diabetic retinopathy.
XX
OS   Homo sapiens.
XX
PN   WO200059947-A1.
XX
PD   12-OCT-2000.
XX
PF   07-APR-2000; 2000WO-US009047.
XX
PR   08-APR-1999;  99US-128711P.
PR   12-JUL-1999;  99US-143992P.
PR   07-JAN-1999;  99US-0114796.
PR   22-DEC-1999;  99US-0171505.
XX
PA   (GENM-) GENENTECH INC.
XX
PI   Kendall RL, Alderson R, Meister B, Reinhardt V, Peters MS;
XX
DR   WPI; 2000-632862/48.
DR   N-PSDB; AAA52093.
XX
PT   Treating injury or degeneration of photoreceptors -
PT   administering to a subject vascular endothelial growth factor -
PT   (VEGF 2)
XX
PS   Claim 41; Fig 1a or 2Bpp; English.
XX
CC   Administration of vascular endothelial growth factor 2 (VEGF 2)
CC   to a patient can be used for treating injury or degeneration of
CC   photoreceptors associated with cystoid cotton wool spots, retinitis
CC   pigmentosa, age related macular degeneration, diabetic retinopathy.
CC   VEGF 2 promotes angiogenesis, the formation of new blood
CC   vessels in the retina.
XX
SQ   Sequence  419 AA;


  Query Match             87.8%;  Score 2049;  DB 2;  Length 419;
  Best Local Similarity   85.0%;  Pred. No. 4.7e-150;
  Matches  354;  Conservative   27;  Mismatches   59;  Indels    4;  Gaps    1;

Qy        1 MNFLLTWVHLVALLLALFSHLIQAVHGCDKPSLMHYLKQPHAEFMASFHKHEAQKIDVAK 60
            |||| |:|||||:|||| |||||  |||| || ||||  |:||  |  |:|| |:|:|
Db        1 mhsigttsvacslmaallqsgfmgapvpqdpalsmslgeetirlmaaqtaaqdgldvtv 60

Qy       61 KSVSSVMVTIMSVVCSCMRK-SRGKLFFVNFVDMEQTCRFSCSAISGTEGQPQASDAGSQ 119
            ||:|||||||:|  |:|||||:|||||||      |:|||:||||||  |||||||||||
Db       61 esvssvdelatiypeywkmykspfikgaltvwphatgdpnkmflethlksvnevlhpdqe 120

Qy      120 SIDNEWPEQWCMEHVTIDVGREAGNLTFAHCNLRVDRMQLMCSKNNSMDWRDSWIIYPPS 179
            |||||||||:|||||||||:|:|:|| ||||:|||||:|||||:|||||:|||:|:|:|
Db      121 sidnewrktpqpqqqldvnktetvatntikpqevevgntlnlcpvnfnrvkitwyfdgqe 180

Qy      180 YHGMKISKYIQDHGTTCLASIFLAPEKPGFIPVLGETIKGSTEDSIWVLCDTPLEEPEIE 239
            |||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 yhgmkisky-qdhgttclasifiapekpgfipvlgetikgstedsiwvlctdpleepeie 239

Qy      240 LVHKKAEEGDLKTPSTHVTFSDLGVKDGELAFRQHLSYFETRIAEELALKRELVEGTEKN 299
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 lvhkkaeegdlktpstHvtfsdlgvkdgelafrqhlsyfetriaeelalkrelvegtekn 299

Qy      300 CHEELAERVETHLHKLEEESDKMRASMQYVVEHLKGQFSSKNLEVDMSAPKDTYVRCLQE 359
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      300 cheelaervethlhkleeesdkmrasmqyvvehlkgqfssknlevdmsapkdtyvrclqe 359

Qy      360 DQSTQIGYCKPMTEFLSEEGISIPEDMDQEAGGLEASVTSHWQREGAELVMSVQGYHIRS 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      360 dqstqigyckpmtefLseegisipedmdqeaggleasvtshwqregaelvmsvqgyhirs 419

Search completed: February 23, 2002, 1:25:45
Job time: 414 sec
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GenCore version 4.5
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Mpi.Prot: protein Search, Gotoh sw model

Run: 5: February 20, 2002, 19:27:58 ; Search Time 1.51 Seconds
(without alignments)
1411.726 Million cell updates/sec

Title: US-09-534-376A-13
Perfect score: 2454
Sequence: 1 MHLLEMLSLGQCLAAGAVLL.....LLAEPVPLVPLSWKSGLMN 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1735053 seqs, 1462723293 residues

Total number of hits satisfying chosen parameters: 1735053

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

* Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2342	99.5	418	13	o57352	o57352 Coturnix co
2	1779	75.6	420	6	Q9XS50	Q9XS50 Bos taurus
3	627	26.8	354	4	o43915	o43915 Homo sapien
4	606	25.8	358	11	P97346	P97346 Mus musculu
5	586.5	25.0	426	11	o35251	o35251 Rattus norv
6	556	23.9	126	11	o35252	o35252 Rattus norv
7	252	9.9	1698	5	Q94448	Q94448 Caenorhabdi
8	231	9.8	1294	5	Q94446	Q94446 Caenorhabdi
9	211.5	9.0	252	4	Q9H1W9	Q9H1W9 Homo sapien
10	211.5	9.0	254	4	Q16889	Q16889 Homo sapien
11	202.5	8.6	208	6	Q9XSF4	Q9XSF4 Canis famil
12	202	8.6	209	4	o60720	o60720 Homo sapien
13	199.5	8.5	214	6	Q9XSF5	Q9XSF5 Canis famil
14	198.5	8.4	214	6	Q9MYV8	Q9MYV8 Canis famil
15	196	8.3	122	5	Q96CLX1	Q96CLX1 Homo sapie
16	194.5	8.3	190	6	Q9XSF3	Q9XSF3 Canis famil
17	193.5	8.2	190	6	Q96KB0	Q96KB0 Equus caba
18	186.5	7.9	190	6	Q96G52	Q96G52 Sus scrofa
19	186.5	7.9	190	11	Q9QX89	Q9QX89 Sparax zos
20	184	7.8	191	4	o75825	o75825 Homo sapien
21	184	7.8	194	13	o42572	o42572 Xenopus lae
22	183.5	7.8	174	4	Q96DZ3	Q96DZ3 Homo sapien
23	180.5	7.7	198	6	o77643	o77643 Ovis aries
24	175	7.4	121	4	Q96HW8	Q96HW8 Homo sapien
25	174.5	7.4	214	12	Q9QX67	Q9QX67 Rattus norv
26	174	7.4	198	11	Q99PS1	Q99PS1 Mus musculu
27	172	7.3	247	4	Q96HC8	Q96HC8 Homo sapien
28	170.5	7.2	1287	2	Q49549	Q49549 Mycoplasma
29	170	7.2	142	11	Q9EK16	Q9EK16 Mesocricetu
30	169.5	7.2	188	13	o73682	o73682 Brachydanio
31	167.5	7.1	124	6	Q96GK00	Q96GK00 Callithrix
32	167.5	7.1	150	11	o54881	o54881 Rattus norv
33	165.5	7.0	314	5	Q96BX1	Q96BX1 Drosophila
34	164.5	7.0	704	8	o74567	o74567 Trichoderma
35	164	6.9	126	6	Q96BB7	Q96BB7 Macaca mula
36	163.5	6.9	188	6	Q9XS49	Q9XS49 Bos taurus
37	161.5	6.9	361	5	Q9VWI9	Q9VWI9 Drosophila
38	158.5	6.7	118	6	Q9MZB1	Q9MZB1 Ovis aries
39	156.5	6.6	148	13	o42571	o42571 Xenopus lae
40	156.5	6.6	170	11	Q9QKX7	Q9QKX7 Rattus norv
41	156.5	6.6	800	5	Q9V878	Q9V878 Drosophila
42	152.5	6.5	146	11	Q9QX36	Q9QX36 Rattus norv
43	152.5	6.5	663	5	o44247	o44247 Hordeum vul
44	151	6.4	123	6	Q9N1S1	Q9N1S1 Cupiennius
45	149.5	6.4	170	4	Q9BV78	Q9BV78 Homo sapien

ALIGNMENTS

RESULT 1
o57352
ID o57352 PRELIMINARY; PRT; 418 AA.
AC o57352;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN VEGF-C.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167966; PubMed=9435294;
RA Eichmann A., Corbel C., Jaffredo T., Breant V., Dunon-Z V., Kumar V.,
RA Altabia K., le Douarin N.M.;
RT "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT of the differentiation of VEGFR2 expressing endothelial cell
RT precursors.";
RL Development 125:743-752(1998).
DR EMBL; Y15837; CAA75799.1; -.
DR HSSP; P15692; 1VPF.
DR InterPro; IPR002460; GF cysknot.
DR InterPro; IPR000426; Glyco hormone.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00456; GDCYSKNT 1.
DR Prodom; PD001629; PDGF; 1.
DR SMART; SM00067; GHA; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 111 418 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ SEQUENCE 418 AA; 46849 MW; 99B1C927915IBE2B CRC64;

Query Match 99.5%; Score 2342; DB 13; Length 418;

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DR   EMBL; D89628; BAA14602.1;  -.
DR   HSSP; P15692; 1VPF.
DR   MGD; MGI:108037; Fgf1.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   458 AA;  51969 MW;  66668B7EBF070457 CRC64;


  Query Match             28.3%;  Score 666;  DB 11;  Length 458;
  Best Local Similarity   39.4%;  Pred. No. 1.7e-56;
  Matches  135;  Conservative   57;  Mismatches   96;  Indels   42;  Gaps    9;

Qy      56 EEQLRSVSSVEEEMEVLYEEYWKMFKPQLRKGGWQHNEEHSSSDIRSHE- SLKEAAAHY 114
           |:|:|: |:::|| : : | |:::|:|        :  :| |:||    | :|:|| |
Db      46 EQQIPAASSLEEELQYIAHSEDWKFTWF-PLELE-----KFSLASMDSRSASHRSTRFAAIEY 99

Qy     114 NAEILKSHIPETWKPSYEQMPPEVQYLGEFCALPNIEEVRDHFQVLVSLGVQECFDKFSVSY 173
           : | || || |:::|| :|| |:|  | | :|||:|:|||:::::|:|||| | | :|
Db     100 DIEILEVIDEEWQQTQKSPKELTTVEVASELQKLNIEFKEPF-VNVFKQGGQNEDGVMQM 159

Qy     174 NISINYIGKEILEIIVPLCHEFEFVIVGIANHIQ-KRSKELDVYRQVHSITRKSLIFA-IQ 232
           | |:|:|| | |:::|:  |: | | |||| |:|:     | :| |||:    :
Db     160 NISISYISKQLEEISVPLISVPELVEVKVANHIQ-KRCLPIQP- RHPVSITRKSIQIEE 217

Qy     233 IQ-HVANKIFPKNHVWNNQ-E-K-LAQHEFSGGHRSPTSGGHITSGENKEIDEEIQQT 290
           :|  : | || : :|:|  |:|: | :    :  :
Db     218 DE-PHSKKLVTIDMEWENIEQ-EGVIQLEIPL      ---          EGIF      276

Qy     291 V-PP- VPPIS-TPPKELDAS-Q-M-ENKEIIS- -ENKEEIEEP-2VVPPIP-EEHHPL 347
                   | |                 ;: |||:  ||||:|:|||  :|
Db     277 ----  ----DHSYIQE--          -- PIEGPHMIEDEDRCE-VCKAP-GGLIQ 308

Qy     348 NPAE-IC EEIESENE-FLECEEEHHQIC-SCYRPP-IVPIKRC 394
           :|  | | || :|  | | | ||  ||||    |  |: |
Db     309 EPEN-S-FE-KESLES-QQKHKIFHEIDSC EDR-PFHIEIC 350


RESULT   5
Q05251
ID   Q05251      PRELIMINARY;      PRT:   326 AA.
AC   Q05251;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN   VEGFD.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=97439118; PubMed=9205122;
RA   Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT   "Molecular cloning of a novel vascular endothelial growth factor,
RT   VEGF-D.";
RL   Genomics 42:483-488(1997).
DR   EMBL; AF014827; AAB66557.1;  -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   326 AA;  37112 MW;  12618FA473596C00 CRC64;
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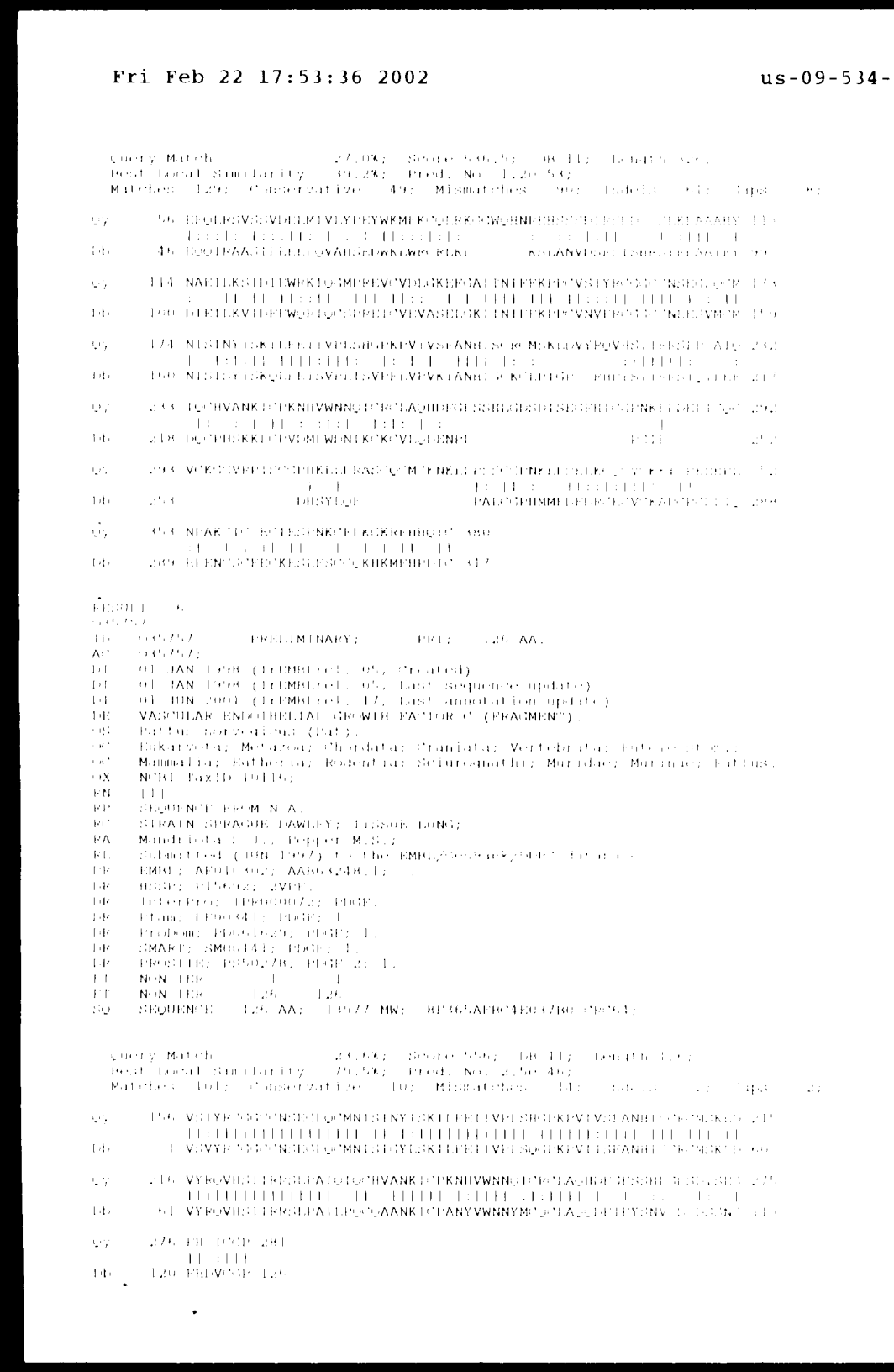

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RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin L., Hamilton R.;
RL   Submitted (APR 1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U54641; AAA99804.1; -.
DR   InterPro; IPR000561; EGF like.
DR   InterPro; IPR000853; Mtllthion_nemat.
DR   PRINTS; PR00876; MTNEMATODE.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ   SEQUENCE   1764 AA;  185745 MW;  3A3F20247C8F1126 CRC64;

  Query Match             9.8%;  Score 231;  DB 5;  Length 1764;
  Best Local Similarity   19.5%;  Pred. No. 1.8e-13;
  Matches   93;  Conservative   58;  Mismatches  192;  Indels  122;  Gaps   17;

Qy         39 EEEPGAGEPKAHAGKLLEEQLLEGVSCVLELMIVLYPEYWKMFK [illegible] 98
Db        963 DEMQNCKSPKAWSHD [illegible] KNADPADECVA--PQTWLENQC  K [illegible] 1016

Qy         99 DIRSDDSLEEAAAHYNAEILKSIDIEWKKIQC---         MPEEV [illegible] K      141
Db       1017 ENKEP [illegible] VCKCP  MESVIPE [illegible] KEWNNEI [illegible] 1074

Qy        142                 EEGALINIEEKPPCVSIYR      [illegible] NSE [illegible] MNISIN 178
Db       1075 PQVNINCPAKQIFIESECEC [illegible] ET---RFKCLDGERFSNLE [illegible] 113

Qy        179 YISKILFEEIVP          ------LSHGFKEVI     VSIANHESC [illegible] MSKI [illegible] 217
Db       1131 [illegible]

Qy        218 RQV       HSIIRRSLPAIQIQCHVAN---------      KTCPKNHVWNN [illegible] 252
Db       1191 KEE [illegible] 1250

Qy        253 [illegible] CLAQHDFGFSSHLGDSDISLGEHD [illegible] GENKELDEE [illegible] 312
Db       1251 CQCVC      ---PENMEEPAPN [illegible] NEWWNDEA [illegible] 1298

Qy        313 [illegible] 366
Db       1299 DACECPPGEAIEA [illegible] 1356

Qy        367 [illegible] YRPP [illegible] VRIKRCDAGFLLAEEV [illegible] V 409
Db       1357 QIC [illegible] FAGQSWDSQICQCSC    ATGP [illegible] FWCAE [illegible] V 1394

RESULT 9
Q9HIW9
ID   Q9HIW9      PRELIMINARY;      PRT;   232 AA.
AC   Q9HIW9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   [illegible] (VASCULAR ENDOTHELIAL GROWTH FACTOR).
GN   VEGF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Williams S.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136131; CAC19512.1; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   232 AA;  27042 MW;  FB49F364446F4[illegible] CRC64;

  Query Match             9.0%;  Score 211.5;  DB 4;  Length 232;
  Best Local Similarity   24.2%;  Pred. No. 1.4e-12;
  Matches   68;  Conservative   33;  Mismatches  105;  Indels   75;  Gaps   10;

Qy         68 [illegible] SIEEAAAHYNAEILKSIDIEWKK 127
Db         14 LLLYLHHAKWSQAAPMAEGGGQNHH-----------              EVVKFMDV YQR 49

Qy        128 IQCMPREVCVI [illegible] KEPCATINIEEKPPCVSIYRC [illegible] NEEI [illegible] MNISINYISKILFEI 187
Db         50 SY [illegible] IETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRI 109

Qy        188 IVPLSHGPKPVIVCIANH [illegible] VYRQVRS [illegible] CHVANKT [illegible] PKNHV 247
Db        110 KP  HQGQHIGEMS [illegible] HNKCECRPKKDRARQ [illegible] CRYKS   162

Qy        248 WNNQI  CRCLAQHDFGFSSHLGDSDISLGEHDCGPNKE         LDEEI [illegible] VCKCVR 299
Db        163 WSVYVGARC [illegible] LM   -----    PWSLPGPHPCGPCSERRKHLFVQ [illegible] K      207

Qy        300 PIS [illegible] RELIRAC [illegible] MCENKLFPS [illegible] NKEFEEKCQC  340
Db        208                  NTDSRCKARQL         ELNERTCR  227

RESULT 10
Q16889
ID   Q16889      PRELIMINARY;      PRT;   254 AA.
AC   Q16889;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
GN   VEGF 206.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92168017; PubMed=1791831;
RA   Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;
RT   "The vascular endothelial growth factor family: identification of a
RT   fourth molecular species and characterization of alternative splicing
RT   of RNA.";
RL   Mol. Endocrinol. 5:1806-1814(1991).
DR   EMBL; S85192; AAC63102.1; -.
DR   EMBL; S85224; AAC63101.1; -.
DR   EMBL; S85196; AAC63101.1; JOINED.
DR   EMBL; S85201; AAC63101.1; JOINED.
DR   EMBL; S85219; AAC63101.1; JOINED.
DR   EMBL; S85222; AAC63101.1; JOINED.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   254 AA;  29461 MW;  069DFE9B9723DBAE CRC64;

  Query Match             9.0%;  Score 211.5;  DB 4;  Length 254;
  Best Local Similarity   24.2%;  Pred. No. 1.6e-12;
  Matches   68;  Conservative   33;  Mismatches  105;  Indels   75;  Gaps   10;

Qy         68 LMIVLYPEYWKMFK [illegible] SIEEAAAHYNAEILKSIDIEWKK 127
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Db      96 LLLEYLHHAKWSQAAFMAESSSQGNHH                          EVVKFMDVYQK 131

Qy     128 IqQMPKFEVFVGQEGKEPGALTNIFEPKPPGYMSIYRPGASQLNRSDTDIYSTLELPKT 187
           :   : :   :: ::       ::: :: : ::::::: ::::::    : :  :  :
Db      72 SYSFIDKEERAVRRIQGLEASGIELYYIDKTQKSVFEMEDYEGFPEPRSIKGVKAHLVGI 131

Qy     188 IVFLSDETGFKFKYKLVSEGVAGMESDYNPQLLVFAAGGIHGVTKPLKFSTGGIDVYDWT 247
           :   :::  :  :  :  :  :  :  ::  :  :  :  :  :  :  :  :  :  :
Db     132 KPIHQSQTETGEMSFDFQHNKCECRPKKDRARQENPCGPCSERRKHLFVQDPQTCKCSCK 191

Qy     248 WNNQLVCPLAQMEGQSSHLGIGDIESDGIFHEGGFQISTVEKSVWTLPKNIE 299
           :  :  ::                :  : : :::  :  :  :  :  :  :
Db     192 NTDSRCKARQLELNERTCRCDKPRR 217

RESULT 11
Q9XSF4
ID   Q9XSF4       PRELIMINARY;      PRT;   208 AA.
AC   Q9XSF4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR (Fragment).
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Jinshiba L., Roque R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF134249; AAD26084.1; -.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   208 AA;  24400 MW;  CF77A5C1EF5C7B8E CRC64;


  Query Match             8.6%;  Score 202.5;  DB 6;  Length 208;
  Best Local Similarity   24.0%;  Pred. No. 9.5e-12;
  Matches   58;  Conservative   28;  Mismatches   77;  Indels   73;  Gaps    7;

Qy     112 HYNAEILKSIDIEWKKIqQMPKFEVFVGQEGKEPGALTNIFEPKPPGYMSIYRPGASQLNRSDTDIq 171
           |   |:::| :|  ::::   | |  || :|:        ||| || : |||:|:| |||:
Db      84 HKPHEVVKFMDVY QQKSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRI 159

Qy     172 QMNISINYISKIFEPEIIEVPLSHGCEKPVIVSPANHISCKHMSKHLVYRQVHSIIRRSLPATLPQCQAA 241
           |  :|  :  :|  :  :  :    |    :||  |: | |  |  |  |  |:  ||  :
Db     160 VPIEEFENITMQITMPKIKPHQAQGHIGEMSFLQHSKCECKPKKDRARQENPCGPCSERRKHLFVQDPQTCKCSCK 239

Qy     242 QTQCHVANKICPKNHVWNNQLCRCLAQHIDEGFSSHLGIGDIESDGIFHEGGFQISTVEKSVWTLPKNIE 299
           : |     :: |                                  |||
Db     240 KQLKPKKPKKKSMP                                 -CSCKSLERKHLFVQDPQTCKCSCK 288

RESULT 12
O60720
ID   O60720       PRELIMINARY;      PRT;   209 AA.
AC   O60720;
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DT   01-APR-1998 (TrEMBLrel. 07, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VEGFB167 PROTEIN PRECURSOR (VASCULAR ENDOTHELIAL GROWTH FACTOR B67)
DE   (VEGF-B167) (VASCULAR ENDOTHELIAL GROWTH FACTOR B67).
GN   VEGFB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=97070474; PubMed=9787057;
RA   Lei L., Jiang A., Pei D.;
RT   "Identification and characterization of a new splicing variant of
RT   vascular endothelial growth factor: VEGF167.";
RL   Biochim. Biophys. Acta, Gene Struct. Expr. 1443:400-405(1998).
RN   [2]
RP   SEQUENCE OF 114-209 FROM N.A.
RC   TISSUE=PLACENTA;
RA   Jingushi L., Roque R.S.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Williams S.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ104438; CAA09179.1; -.
DR   EMBL; AF095445; AAC16730.1; -.
DR   EMBL; AJ136614; CAB19614.1; -.
DR   HSSP; P15692; 2VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Signal.
FT   SIGNAL          1     20       POTENTIAL.
FT   CHAIN          21    209       VEGFB167 PROTEIN.
SQ   SEQUENCE   209 AA;  24422 MW;  F010CCEACD945D6CA CRC64;


  Query Match             8.6%;  Score 202;  DB 4;  Length 209;
  Best Local Similarity   22.5%;  Pred. No. 1.1e-11;
  Matches   63;  Conservative   29;  Mismatches   92;  Indels   90;  Gaps    9;

Qy      98 LMEVYTEYWKMFKQQLEKKGQWQHNKEHSSSSDIESDGSLKLAAARYNAEILKSIDIEWKK 157
           |:  :|  :  |          || |:                  |:::| :|  :::
Db      14 LLEYLHHAKWSQAAFMAESSSQGNHH                    EVVKFMDVYQK 60

Qy     158 IqQMPKFEVFVGQEGKEPGALTNIFEPKPPGYMSIYRPGASQLNRSDTDIYSTLELPKT 217
           |  :|  :  :|  :  :  :    |    :||  |: | |  |  |  |  |:  ||  :
Db      61 SYSFIDKEERAVRRIQGLEASGIELYYIDKTQKSVFEMEDYEGFPEPRSIKGVKAHLVGI 120

Qy     218 IVFLSDETGFKFKYKLVSEGVAGMESDYNPQLLVFAAGGIHGVTKPLKFSTGGIDVYDWT 277
           :   :::  :  :  :  :  :  ::  :  :  :  :  :  :  :  :  :  :
Db     121 KPIHQSQTETGEMSFDFQHNKCECRPKKDRARQENPCGPCSERRKHLFVQDPQTCKCSCK 180

Qy     278 WNNQLVCPLAQMEGQSSHLGIGDIESDGIFHEGGFQISTVEKSVWTLPKNIE 329
           :  :  ::                :  : : :::  :  :  :  :  :  :
Db     181 NTDSRCKARQLELNERTCRCDKPRR 206

RESULT 13
Q9XSF5
ID   Q9XSF5       PRELIMINARY;      PRT;   214 AA.
AC   Q9XSF5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
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SC   21-NOV-1999 (IrEMBLrel. 12, Last Sequence update)
DT   15-JUN-2001 (IrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 188.
GN   VEGF.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RT   "Cloning and characterization of canine vascular endothelial growth
RT   factor.";
RA   Spanjaard R.A., Roque R.S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF143250; AAD29084.1; -.
DR   PIR; PT5692; PT5692.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
SQ   SEQUENCE   214 AA;  25151 MW;  226C0B1AEB5C1C3C CRC64;

  Query Match             8.5%;  Score 166.5;  DB 6;  Length 214;
  Best Local Similarity   25.0%;  Pred. No. 1.2e-11;
  Matches   53;  Conservative   40;  Mismatches   89;  Indels   74;  Gaps    8;

Qy     112 HYNAEILKSIDIEDWKKIQPSMPRYVYVDLGKEEQTAIINIFKPPQRVSIYRCTCNRPGL 171
           |   |:|| :|  |:::   | | |:  :|:        ||| :| : |:|| | :|
Db      43 HKIHSVVKEPMDV YQFSYCGKCSKKLTRFYVQFSFRDVNWGRWIIAPKGYNANYCHGE 102

Qy     172 CMNISINYFKKSDLECIPTYRPSSYKFVSVSTANTNQKMYSHWLGVFSQNSGFTKYGFAGL 231
           |  :|   | :|  :  :  :   |    :|| |:| | |  |  ||    ||
Db     103 CVPIEETSMTIIDIVNGNNIAKYIFSNIRPNVEAVPLPPSYIGALFLLDENETVGTDFRWR 162

Qy     232 QFSQCVKVANKTSRNSVNNQVFVKLAGHEFESSHEQDSHSISPSTSEIHQTFNKEIKEPCQ 291
                                                          |  ::   :
Db     163                    ----                      --        GKSQKEKRKR    195

Qy     292 CVCKGVRGISSVKDALKKLEAMSGTLRTASQQMLKNKLKSFLNPAPFEEIKRVC 345
           |   :|  : |||  |          :  :|:|:|:    |:   :   :|  :||
Db     196 KSEYEFQWSVPQGAPSEKKHLEVGETQTLRVRRGQRLKPEHPAPNIFKDQLAE 249

RESULT  15
Q9GLX1
ID   Q9GLX1      PRELIMINARY;      PRT:   122 AA.
AC   Q9GLX1;
DT   01-MAR-2001 (IrEMBLrel. 16, Created)
DT   01-MAR-2001 (IrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (IrEMBLrel. 17, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR 1 (FRAGMENT).
GN   VEGF-D.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Mandriota S.J., Pepper M.S.;
RL   Submitted (01-MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF099135; AAG29747.1; -.
DR   InterPro; IPR000072; PDGF.
DR   ProDom; PD001629; PDGF; 1.
FT   NON_TER       1       1
FT   NON_TER     122     122
SQ   SEQUENCE   122 AA;  13820 MW;  0C504B0092D054EB CRC64;

  Query Match             8.4%;  Score 156;  DB 6;  Length 122;
  Best Local Similarity   27.2%;  Pred. No. 2.2e-11;
  Matches   47;  Conservative   27;  Mismatches   45;  Indels   54;  Gaps    6;

Qy     187 IIVPLSHEPEPVIVSFANDIGFDMSECAVYEQVHSIIRRSLI AIGILCHVANKYTPKN 247
           |:|||: :: | |  : |: |:         |  |||||:    :  :  : | |
Db       1 ISVPLISVPELVPVKVANHIGCKCFPIAP KHPESIIRRSIQIPEEDRCSHSKKLCPVE 59

Qy     248 DVWNMITLCKHTGAGHEVGGEGVEGETVKMSSNGELVYSKTVKDLVCLGCTGMLVGPQSL 307
           :|:|  |: : |  :                  |   ::: :
Db      60 MEARSNKCKCVLAPE                 NPLACMEDHI                 88

Qy     308 RTNTECQCVCRNTTDPHPLMHNRAKP 357
           | :||          : || : :|||:|:|||| |||:   :|  |
Db      89 HIALPL               AIGMGMKSIELRRCKCVCKTPCPRNPIDKGSVEN 121

Search completed: February 22, 2002, 16:27:09
```

SM protein - protein search, using sw model

Run on: February 20, 2002, 16:27:32 ; Search time 17.05 Seconds
(without alignments)
898.355 Million cell updates/sec

Title: US-09-534-276A-13
Perfect score: 2454
Sequence: 1 MHLLEMLSLGCCLAAGAVLL.....LLAEEVCRCVPISWKRPLMN 419

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1804.5	76.7	419	1	VEGC_HUMAN	P49767 homo sapien
2	1747.5	74.2	415	1	VEGC_MOUSE	P97953 mus musculu
3	241	10.2	1709	1	BAR3_CHITE	Q21328 chitobacte
4	199	8.5	215	1	VEGF_HUMAN	P15692 homo sapien
5	191.5	8.1	190	1	VEGF_PIG	P19151 sus scr ia
6	188.5	8.0	190	1	VEGF_RAT	P50612 rattus norv
7	179.5	7.6	164	1	VEGF_CAVPO	P26617 cavia porce
8	179.5	7.6	190	1	VEGF_BOVIN	P15691 bos taurus
9	174.5	7.4	214	1	VEGF_MOUSE	Q00731 mus musculu
10	169	7.2	216	1	VEGF_CHICK	P52592 gallus gall
11	164.5	7.0	188	1	VEGB_MOUSE	P49766 mus musculu
12	162.5	6.9	188	1	VEGB_HUMAN	P49765 homo sapien
13	158.5	6.7	146	1	VEGF_SHEEP	P50412 ovis aries
14	152	6.5	2871	1	FBN1_MOUSE	Q61554 mus musculu
15	150	6.4	148	1	VEGB_ORFNZ	P52585 ort virus (
16	147.5	6.3	170	1	PLGF_HUMAN	P49763 homo sapien
17	147	6.2	2871	1	FBN1_PIG	Q61555 sus scrofa
18	146.5	6.2	133	1	VEGH_ORFN2	P52587 ort virus (
19	144	6.1	2871	1	FBN1_HUMAN	P35555 homo sapien
20	141.5	6.0	3712	1	LMA_DROME	Q01974 drosophila
21	141	6.0	390	1	SEPT_MOUSE	P52735 mus musculu
22	140	5.9	2871	1	FBN1_BOVIN	P98133 bos taurus
23	138	5.9	837	1	MUC1_RAT	P98089 rattus norv
24	137.5	5.8	1104	1	NFX1_HUMAN	Q12986 homo sapien
25	137.5	5.8	1964	1	NTN4_MOUSE	P58137 mus musculu
26	136.5	5.8	473	1	FP2_MTIGA	Q27054 mytilus gal
27	136.5	5.8	1808	1	TENA_CHICK	P10039 gallus gall
28	135	5.7	2338	1	NTN4_MOUSE	Q61392 mus musculu
29	134.5	5.7	2201	1	TENA_HUMAN	P24821 homo sapien
30	134	5.7	2703	1	NOTC_DROME	P07207 drosophila
31	133.5	5.7	810	1	NEL1_RAT	Q62910 rattus norv
32	132.5	5.6	810	1	NEL1_HUMAN	Q92832 homo sapien
33	132	5.6	827	1	NEL1_MOUSE	Q62911 mus musculu
34	132	5.6	2813	1	VWF_CANFA	Q28295 canis fami
35	131.5	5.6	2531	1	NTN1_MOUSE	Q61390 mus musculu
36	131	5.6	158	1	PLGF_MOUSE	P47964 mus musculu
37	129.5	5.5	1106	1	SPC_DROME	P40798 drosophila
38	129.5	5.5	1408	1	SERR_DROME	P18168 drosophila
39	128	5.4	2813	1	VWF_HUMAN	P04275 homo sapien
40	128	5.4	4051	1	YNX3_CAEEL	P34576 caenorhabdi
41	128	5.4	5376	1	ZAN_MOUSE	Q88799 mus musculu
42	127	5.4	1429	1	LIF2_CAEEL	P34585 caenorhabdi
43	126.5	5.4	241	1	PDGB_SHEEP	Q95229 ovis aries
44	126.5	5.4	1877	1	P'K5_MOUSE	Q64592 mus musculu
45	126	5.4	575	1	TRBM_HUMAN	P07204 homo sapien

ALIGNMENTS

RESULT 1
VEGC_HUMAN
ID VEGC_HUMAN STANDARD; PRT; 419 AA.
AC P49767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4
DE L).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX MEDLINE=96178224; PubMed=8617204;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RT "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL EMBO J. 15:290-298(1996).
RN [2]
RP ERRATUM.
RX MEDLINE=96203094; PubMed=8612600;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RL EMBO J. 15:1751-1751(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96412526; PubMed=8700872;
RA Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RT "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Fowler P.S., Jiang A.J., Greco R.,
RA Burgess P., Giannotti J., Charletta A., Hennessey D., Kovacic S.,
RA Fitzgerald M., Scarlato H., Welch N., Nobon S., Finnerty H.,
RA Sullivan K., Wang J., Nickbarg E., Gasaway K., Turner K.,
RA Wood C.R.;
RP SUBMITTED (JUN-1995) TO THE EMBL/GENBANK/DDBJ databases.
CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH.
CC ! SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC ! PTM: PROBABLY PROTEOLYTICALLY PROCESSED IN THE C-TERMINUS.
CC ! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -!- ---------- ---------- ---------- ---------- ---------- ----------
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CC
DR   EMBL; X94216; CAA64007.1; -.
DR   EMBL; U43411; AAA85214.1; -.
DR   EMBL; U56111; AAB02609.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 99720; -.
DR   InterPro; IPR000100; GF_cysknot.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GF_CYSKNOT.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL       1      ?       POTENTIAL.
FT   PROPEP       ?     103      POTENTIAL.
FT   CHAIN      104     419      VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN     275     365      4 X 24 AA TANDEM REPEATS.
FT   REPEAT     275     298      1.
FT   REPEAT     299     322      2.
FT   REPEAT     323     346      3.
FT   REPEAT     347     365      4 (PARTIAL).
FT   CARBOHYD   175     175      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   205     205      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   240     240      N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   419 AA;  46883 MW;  9F59B7F9DB85E014F CRC64;
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  Query Match             75.7%;  Score 1004.5;  DB 1;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 2e-144;
  Matches  418;  Conservative   59;  Mismatches   60;  Indels    2;  Gaps    2;

Qy       1 MHLLEMELSLGYCTAAGAVLLGPKQ PPVAAAFESGIDLSDAYRPDAGFAAPPAVARSLRVGL 60
           ||||   |: | | | |:|: ||| | |||:|||    : || ||| |:|||||||||
Db       1 MHLLGFFSVACSLLAAALLPGPREAPAAAAAFESGIDLSDAEPDAGEATAYAAKDLEEQL 60

Qy      61 RGVSSVQELTMLVLYPEYWKMFKCQLRKCCWYRNRRDRSGDQETYCSKEAAATVASELKT 120
           ||||||||||||||||||||||||||||||| :: :::::::: | | :| | |
Db      61 RGVSSVQELTMLVLYPEYWKMYKCQLRKCCWYRNRRDLANLNERLERIEQAASPSGNETVK 120

Qy     121 SSLELNMYNIQSIAGTDSTPEDFVWLDIFDNSQNTDVQSPSSITNDSLQVRLNDSFSSVG 180
           ||| |||||| |||||:|:|||||  |||||||||||:|||||||||||||| || | |
Db     121 GIDNEWRETQMTPQIFVFSTEIGSVGLDCVANLRDRSTQVAYRSRGEIQMNDSLGYIPSH 180

Qy     181 IKTLEPELIVPLSHEGPKPVTVSFANHTSYKMESKLVYNQVIRSGTPCALPETQRGMDNN 240
           ||||||:|||||| |||||:|||||||||||||||||||||||||||||||:| |||   | ||
Db     181 IGKLEPELIVPESQGPRPVTISFANHTSYKMESKLVYNQVIRSGTPCALPETQRGMDNN 240

Qy     241 KLCPKNHVWNNQLCPKCLAQRDPVSSSHLQDSDIFSDGEH DQGENKLLEKLPGVCKSCV 300
           |||| |:||| |||||| || ||  | |:|:|||| ||||||||||||| ||| | |
Db     241 KFCPENYMWNNHICPKCLAQFDPMEQSGEACDSLDITCTHLDEQCNPELLPPQVVDRASL 300

Qy     301 RPISYSGPHKELDRAFSVGMKWMSFNELRLKECKCWGGCSGPKDEDCLRCLKFSKFANDT 360
           || |||||||||| |||:|||| || ||:|||:|||:|||||||||||| |||:|||||||
Db     301 RAASVSGPHKELDRAFSVGMKWMSFNELRLKECKCWGGCSGPKDEDCLRCLKFSKFANDT 360

Qy     361 GACLRESSPNKCFLKCKRFRRHQTSCYVRPPSCLVRTKHRCDAGFTAFEEVGPSVLPNVPK 420
           |||||| || ||||:|||||||||||| ||| | | | :|  :|||||| : | | |
Db     361 GACLRETSFSKCFLKCKKFRRHQTSCYVRPVTCLVRTKHRCDAGFTAFEEVGPSVLPNVPK 420

RESULT   2
VEGFC_MOUSE
ID   VEGFC_MOUSE     STANDARD;      PRT;   419 AA.
AC   P97953;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   30-APR-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND)
DE   (FLT4-L).
GN   VEGFC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=97194697; PubMed=9012504;
RA   Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA   Joukov V., Alitalo K.;
RT   "VEGF-C receptor binding and pattern of expression with VEGFR-3
RT   suggests a role in lymphatic vascular development.";
RL   Development 122:3829-3837(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=97308482; PubMed=9247316;
RA   Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,
RA   Alitalo K., Armstrong E.;
RT   "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like
RT   loops and is expressed in multiple human tumors and endothelia.";
RL   Cancer Res. 52:5738-5743(1992).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR   EMBL; U73620; AAC52984.1; -.
DR   EMBL; U56112; AAB46707.1; -.
DR   HSSP; P15692; 1VPF.
DR   MGD; MGI:106124; Vegfc.
DR   InterPro; IPR000100; GF_cysknot.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   PRINTS; PR00438; GF_CYSKNOT.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
FT   SIGNAL       1      ?       POTENTIAL.
FT   PROPEP       ?     103      POTENTIAL.
FT   CHAIN       104     419      VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT   DOMAIN      275     365      4 X 24 AA TANDEM REPEATS.
FT   REPEAT      275     298      1.
FT   REPEAT      299     322      2.
FT   REPEAT      323     346      3.
FT   REPEAT      347     365      4 (PARTIAL).
FT   CARBOHYD    175     175      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    205     205      N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    240     240      N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   419 AA;  46871 MW;  D9D43DB5C6C5C59D CRC64;

  Query Match             74.2%;  Score 1747.5;  DB 1;  Length 419;
  Best Local Similarity   74.0%;  Pred. No. 3.8e-144;
  Matches  414;  Conservative   57;  Mismatches   66;  Indels    2;  Gaps    2;

Qy       1 MHLLEMELSLGYCTAAGAVLLGPKQ PPVAAAFESGIDLSDAYRPDAGFAAPPAVARSLRVGL 60
           ||||   ||| | | | |:|:  ||| | |||:|| | : || ||  |:|||| | |||||
Db       1 MHLLGCFLSLACSLLAAALLPGPREAPAIVAAFESGLDLSEAERPDAGEVKAPPGKLEERQL 60

Qy      61 RGVSSVQELTMLVLYPEYWKMFKCQLRKCCWYRNRRDRSGDQETYCSKEAAATVASELKT 120
           |||||||||||||||||||||||||||||||| :: :::::::: | | :| | |
Db      61 RGVSSVQELTMLVLYPEYWKMYKCQLRKCCWYRNRRDLANLNERLERIEQAASPSGNETVK 120
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RA   Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT   "Human vascular permeability factor. Isolation from U937 cells.";
RL   J. Biol. Chem. 264:20017-20024(1989).
RN   [6]
RP   SEQUENCE OF 27-41.
RX   MEDLINE=93145046; PubMed=7678805;
RA   Fiebich B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,
RA   Kochs G., Marme D., Hug H., Weich H.A.;
RT   "Synthesis and assembly of functionally active human vascular
RT   endothelial growth factor homodimers in insect cells.";
RL   Eur. J. Biochem. 211:19-26(1993).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX   MEDLINE=97352774; PubMed=9207067;
RA   Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA   de Vos A.M.;
RT   "Vascular endothelial growth factor: crystal structure and functional
RT   mapping of the kinase domain receptor binding site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX   MEDLINE=98035455; PubMed=9351807;
RA   Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT   "The crystal structure of vascular endothelial growth factor (VEGF)
RT   refined to 1.93 A resolution: multiple copy flexibility and receptor
RT   binding.";
RL   Structure 5:1325-1338(1997).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX   MEDLINE=99119204; PubMed=9922142;
RA   Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA   Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT   "Crystal structure of the complex between VEGF and a receptor-blocking
RT   peptide.";
RL   Biochemistry 37:17765-17772(1998).
RN   [10]
RP   STRUCTURE BY NMR OF 34-135.
RX   MEDLINE=97477915; PubMed=9336848;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "1H, 13C, and 15N backbone assignment and secondary structure of the
RT   receptor-binding domain of vascular endothelial growth factor.";
RL   Protein Sci. 6:2250-2260(1997).
RN   [11]
RP   STRUCTURE BY NMR OF 137-215.
RX   MEDLINE=98208446; PubMed=9634701;
RA   Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA   Starovasnik M.A.;
RT   "Solution structure of the heparin-binding domain of vascular
RT   endothelial growth factor.";
RL   Structure 6:637-648(1998).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, VASCULOGENESIS AND ENDOTHELIAL
CC       CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY
CC       ALTERNATIVE SPLICING OF THE SAME GENE (VEGF 121, VEGF 165,
CC       VEGF 189 AND VEGF 215).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR   EMBL; M32977; AAA35789.1; -.
DR   EMBL; M27281; AAA36807.1; -.
DR   EMBL; M63978; AAA36804.1; -.
DR   EMBL; M63971; AAA36804.1; JOINED.
DR   EMBL; M63972; AAA36804.1; JOINED.
DR   EMBL; M63973; AAA36804.1; JOINED.
DR   EMBL; M63974; AAA36804.1; JOINED.
DR   EMBL; M63975; AAA36804.1; JOINED.
DR   EMBL; M63976; AAA36804.1; JOINED.
DR   EMBL; M63977; AAA36804.1; JOINED.
DR   EMBL; X62568; CAA44447.1; -.
DR   PIR; A34492; A34492.
DR   PIR; A40079; A40079.
DR   PIR; A40080; A40080.
DR   PIR; A40454; A40454.
DR   PIR; B40454; B40454.
DR   PIR; C40454; C40454.
DR   PIR; JQ1463; JQ1463.
DR   PIR; JQ1464; JQ1464.
DR   PIR; S17348; S17348.
DR   PDB; 1VGH; 08-APR-98.
DR   PDB; 2VGH; 08-APR-98.
DR   PDB; 1VPF; 08-APR-98.
DR   PDB; 2VPF; 29-JUL-98.
DR   PDB; 1VPP; 23-FEB-99.
DR   MIM; 192240; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal;
KW   3D-structure.
FT   SIGNAL        1     26
FT   CHAIN        27    215       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     52     94
FT   DISULFID     83    128
FT   DISULFID     87    130
FT   DISULFID     77     77       INTERCHAIN.
FT   DISULFID     86     86       INTERCHAIN.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .).
FT   VARSPLIC    141    141       K -> N (IN ISOFORM VEGF 121 AND ISOFORM
FT                                VEGF 165).
FT   VARSPLIC    142    165       MISSING (IN ISOFORM VEGF 165).
FT   VARSPLIC    142    209       MISSING (IN ISOFORM VEGF 121).
SQ   SEQUENCE   215 AA;  25173 MW;  7B975AD[illegible] CRC64;

  Query Match             8.5%;  Score 199;  DB 1;  Length 215;
  Best Local Similarity   22.9%;  Pred. No. 7.6e-09;
  Matches   64;  Conservative   31;  Mismatches   95;  Indels   90;  Gaps    9;

Qy         [illegible] 127
Db         14 LLLYLHHAKWSQAAPMAEGGGQNHH [illegible] EVVKFMDVYQR 49

Qy        128 [illegible] 187
Db         50 [illegible] 109

Qy        188 [illegible] 247
Db        110 [illegible]GKGQKRKRKKSRYKS 142

Qy        248 WNNQ[illegible] 300
Db        163 WSVP[illegible]CGPCSERRKHLFVQDPQTCKCSCK 190

Qy        301 [illegible] 340
Db        191 NTDSRCKARQL [illegible] ELNERTCRC 210


RESULT 5
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VEGF_FIS
ID   VEGF_FIS        STANDARD;      PRT:   190 AA.
AC   P49763;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   20-APR-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VAS  AP
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=94143284; PubMed=7841269;
RA   Sharma H.S., Ismail Z.B., Ghe B.C.H., Verdonw P.D.;
RT   "Nucleotide sequence and expression of the porcine vascular
RT   endothelial growth factor.";
RL   Biochim. Biophys. Acta 1260:245-248(1995).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC       CELL GROWTH, INDUCTION OF ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; AF031445; AAC97414.1; -.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD000225; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GlcNAc...).
SQ   SEQUENCE   190 AA;  22308 MW;  04D40B8D27913047F CRC64;


  Query Match             8.1%;  Score 191.5;  DB 1;  Length 190;
  Best Local Similarity   27.5%;  Pred. No. 2.6e-09;
  Matches   49;  Conservative   44;  Mismatches   78;  Indels   19;  Gaps   3;

Qy      116 EILKSIDIEWFKIIDQWEEEVGKRPRDQAVSIYRSSVQELHKTKSKIVNIKKE 170
            ||| ||  ||||    | |  ||  ||        ||| || | ||||||| ||||  |
Db       98 EVVKEMDV YQKSYCKPEEVGVIYQGLERSTKDTYHKPSYVFLRKSKGDNDGYIEK  151

Qy      171 SIPYIGKEIFEIVEVGPSPKHIYVEFANKSGMSMVGVKSNDHSWMCLGKLYPTVTP 227
            |   | ||  | |  |||  |  |  ||| | | | | ||              | |
Db      152 VIEENHTM DWKFRDLGLQLPCYMTILENKNLSPIAEIWGPLPTPLYLEMLDNYSA  208

Qy      228 HVANKLTPENHVWNNQTPFTLAQHSEIGDSEHRGVMIPQVKNHLMYNKEIFFEEHG 284
            |   |  | | | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      209 GPCSEKRKHLEFNGPQYCKKSL  NITKP  KRAPGGLNPNIS  GP  GMP  232

RESULT   6
VEGF_RAT
ID   VEGF_RAT        STANDARD;      PRT:   190 AA.
AC   P16612;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   20-APR-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-190.
RX   MEDLINE=90207249; PubMed=2320579;
RA   Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
RA   Palisi T.M., Hope D.A., Thomas K.A.;
RT   "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT   that is homologous to platelet-derived growth factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2628-2632(1990).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC       CELL GROWTH, INDUCTION OF ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE FOLLICLE, IN BRAIN, IN
CC       FASCICULATE IN ADRENAL AND PARAVENTRICULAR NUCLEI, AND IN
CC       CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF
CC       THE OVARY AND IN KIDNEY GLOMERULI.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; M32167; AAA41211.1; -.
DR   PIR; A35987; A35987.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD000225; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51     93       BY SIMILARITY.
FT   DISULFID     82    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GlcNAc...).
SQ   SEQUENCE   190 AA;  22396 MW;  5B9374A0104411F477 CRC64;


  Query Match             8.1%;  Score 189.5;  DB 1;  Length 190;
  Best Local Similarity   22.1%;  Pred. No. 4.5e-08;
  Matches   52;  Conservative   41;  Mismatches   98;  Indels   9;  Gaps   2;

Qy       91 RNEEKSNVEIPEYFQELTGAAAKVNALCLAVLMWAVEGDRAVHSTAFINSIF 145
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Db       1  MHAcWsvAAFLvSvgM   Ac   EVVKEMDV YQKSYCKPEEILVGILGEYFDEIFYI 77
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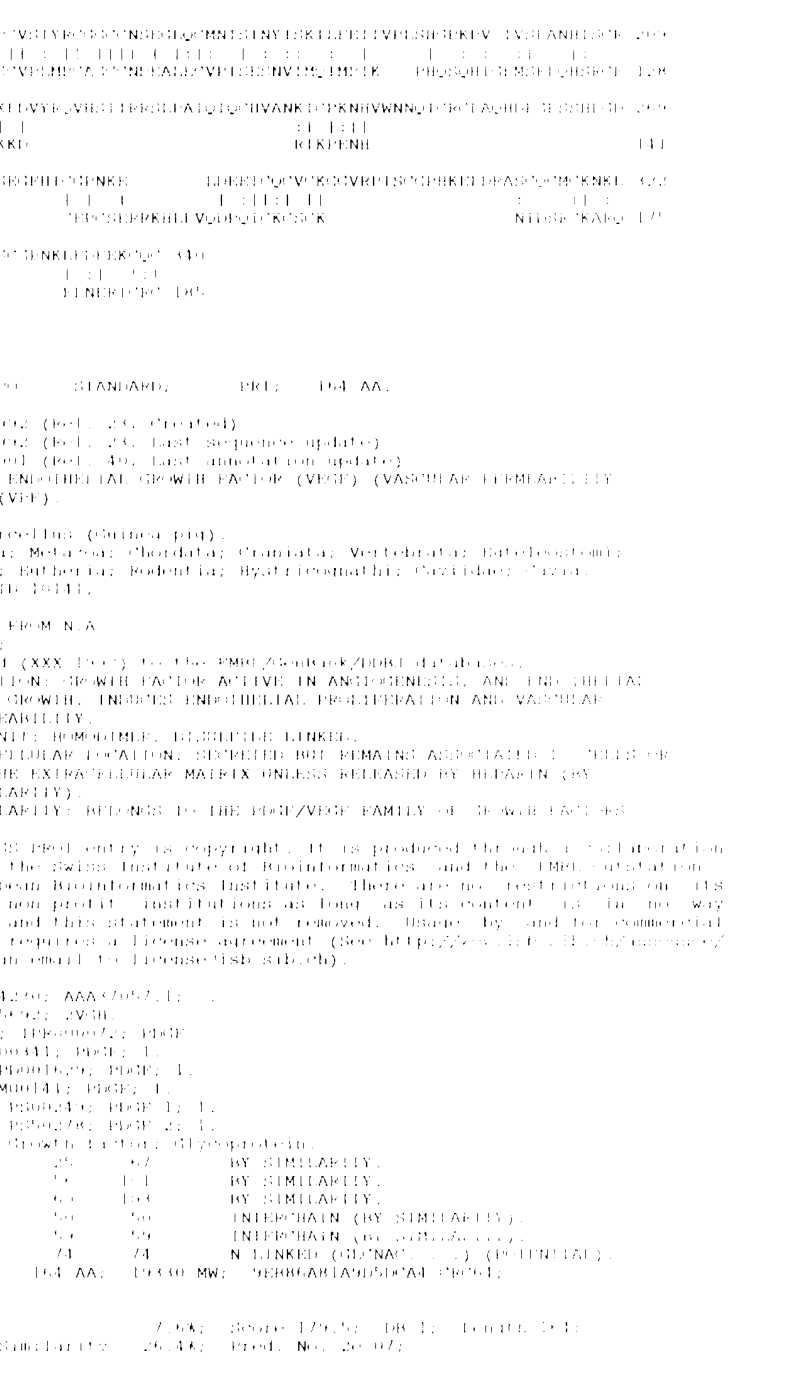

RESULT 7
VEGF_CAVPO
ID VEGF_CAVPO STANDARD; PRT; 164 AA.
AC P29674;
DT 01-APR-1996 (Rel. 34, Created)
DT 01-APR-1996 (Rel. 34, Last sequence update)
DT 29-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY
DE FACTOR) (VPF).
GN VEGF.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Berse B.;
RL Submitted (XXX-1997) to the EMBL/GenBank/DDBJ databases.
CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC ! SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC ! SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC ! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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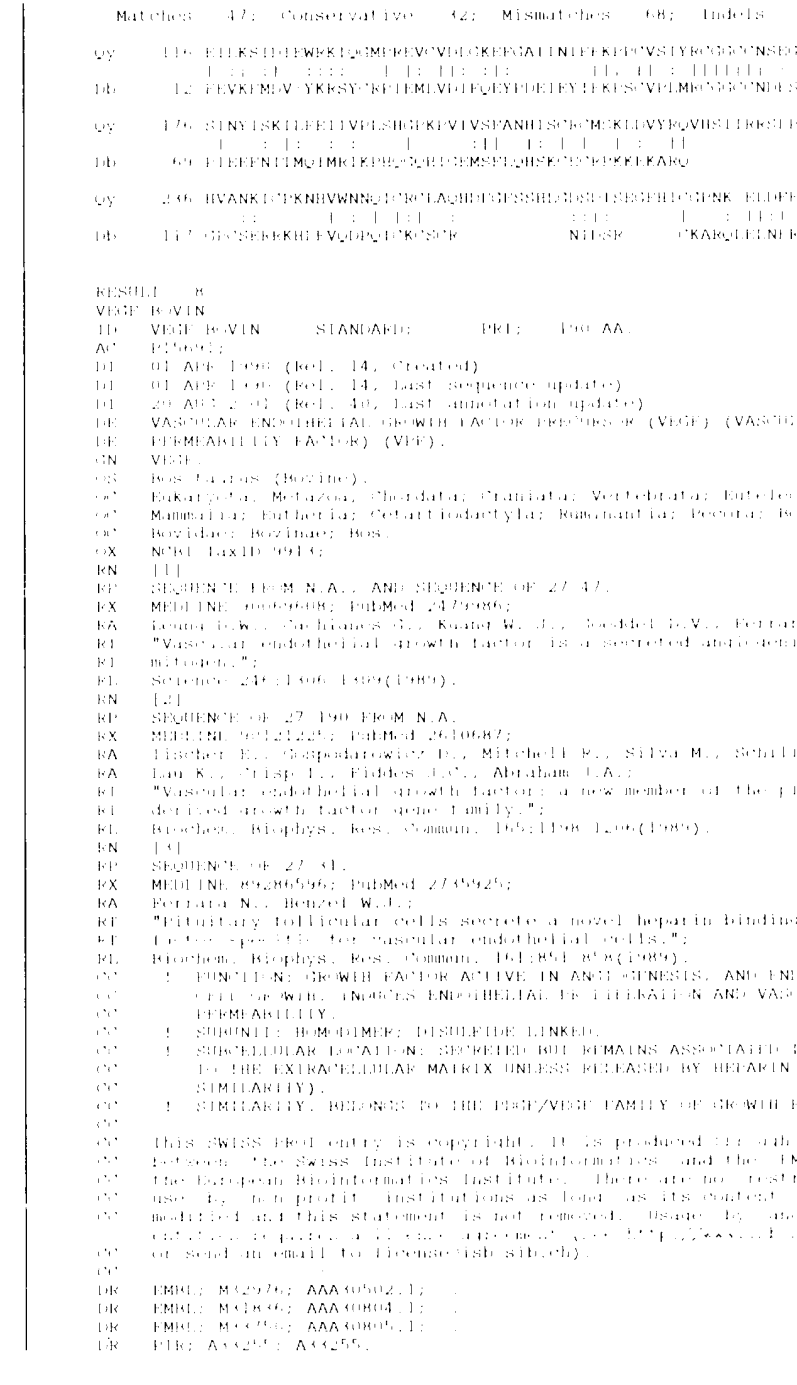
CC
DR EMBL; M32979; AAA40502.1; -.
DR HSSP; P15692; 2VGH.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD000176; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein.
FT DISULFID 25 67 BY SIMILARITY.
FT DISULFID 75 111 BY SIMILARITY.
FT DISULFID 67 104 BY SIMILARITY.
FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT DISULFID 54 59 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 164 AA; 19330 MW; 9EB86ABA9D5DC4AE CRC64;

Query Match 7.9%; Score 17.5; DB 1; Length 164;
Best Local Similarity 26.4%; Pred. No. 2e-07;

Matches 47; Conservative 32; Mismatches 68; Indels 81; Gaps 6;



RESULT 8
VEGF_BOVIN
ID VEGF_BOVIN STANDARD; PRT; 190 AA.
AC P50406;
DT 01-APR-1996 (Rel. 34, Created)
DT 01-APR-1996 (Rel. 34, Last sequence update)
DT 29-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE=96060608; PubMed=7479086;
RA Ferrara N., Carnevale K., Cohen T., Alberts B., Leung D.W.;
RT "Vascular endothelial growth factor is a secreted angiogenic
RT mitogen.";
RL Science 258:1506-1509(1992).
RN [2]
RP SEQUENCE OF 27-190 FROM N.A.
RX MEDLINE=96124225; PubMed=8610847;
RA Fischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,
RA Lau K., Crisp T., Fiddes J.C., Abraham J.A.;
RT "Vascular endothelial growth factor: a new member of the platelet-
RT derived growth factor gene family.";
RL Biochem. Biophys. Res. Commun. 165:1198-1206(1989).
RN [3]
RP SEQUENCE OF 27-41.
RX MEDLINE=89286596; PubMed=2735925;
RA Ferrara N., Henzel W.J.;
RT "Pituitary follicular cells secrete a novel heparin binding growth
RT factor specific for vascular endothelial cells.";
RL Biochem. Biophys. Res. Commun. 161:851-858(1989).
CC ! FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC ! SUBUNIT: HOMODIMER; DISULFIDE LINKED.
CC ! SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC ! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC
DR EMBL; M32976; AAA40502.1; -.
DR EMBL; M61836; AAA40804.1; -.
DR EMBL; M57736; AAA40805.1; -.
DR PIR; A33255; A33255.

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CP   PIR; A43787; A43787.
CP   PIR; B40080; B40080.
DR   BSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001620; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    190       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID      51     93       BY SIMILARITY.
FT   DISULFID      82    127       BY SIMILARITY.
FT   DISULFID      86    129       BY SIMILARITY.
FT   DISULFID      76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID      85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     100    100       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC     146    146       MISSING (IN ISOFORM VEGF-121).
FT   VARSPLIC     147    165       MISSING (IN ISOFORM VEGF-165).
FT   VARSPLIC     147    209       MISSING (IN ISOFORM VEGF-189).
FT   CONFLICT     117    118       GE -> EK (IN REF. 2).
SQ   SEQUENCE   191 AA;  21892 MW;  A5C3A0A9B38F97F3 CRC64;

  Query Match             7.6%;  Score 179.5;  DB 1;  Length 191;
  Best Local Similarity  26.8%;  Pred. No. 2.6e-07;
  Matches   96;  Conservative   40;  Mismatches   63;  Indels   11;  Gaps    8;

Qy      110 EIEKSIQIISGKRKKELKLGHEEKLEGAIVNIEEKFDQVSIYDNSRGELIGSVKNQ 169
            ||:|:||:|:::  ||  ||:||:        ||:||:|:|||||:|:||
Db       38 EVVKEMDVYQRSFCKPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALEC 97

Qy      170 STNYISKLEAWVTVI-----SDGRLKVEHKNGETRDLVISECKTKSTELRHVQSIV 224
                :   |:||:     :  : :  :||  |  :|:|  :|:|
Db       98 ----VETIEETNITMQIMRIKPHQSQHIGEMSFLQHNKCECRPKKDRARQENPCGP 153

Qy      225 EKLLHVANKEIKNAIVWNNKFGVMALFKLSTKSGSLEFMSKRAIQNAIIHVGSRCK 279
            :  :   :  :  :  |:  :  :  :  :  :  :  :  :  :  :  :  :
Db      154 ENPGHFDWSERKKHETVQIPVDLQCNISMK-------NITGR-------EAELIVNCEE 196

Qy      280 GQK 282
            |:|
Db      197 GEK 199


RESULT  9
VEGF_MOUSE
ID   VEGF_MOUSE     STANDARD;      PRT:   214 AA.
AC   P30741;
DT   01-AUG-1993 (Rel. 25, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92274865; PubMed=1569833;
RA   Breier G., Albrecht U., Sterrer S., Risau W.;
RT   "Expression of vascular endothelial growth factor during
RT   embryonic angiogenesis and endothelial cell differentiation.";
RL   Development 114:521-532(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (VEGF 1).
RX   MEDLINE=92355511; PubMed=1644816;
RA   Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT   "Vascular endothelial growth factor. Regulation by cell
RT   differentiation and activated second messenger pathways.";
RL   J. Biol. Chem. 267:16317-16322(1992).
RN   [3]
RP   SEQUENCE OF 1-8 FROM N.A.
RX   MEDLINE=96216498; PubMed=8632907;
RA   Shima D.T., Kuroki M., Deutsch U., Ng Y.S., Adamis A.P., D'Amore P.A.;
RT   "The mouse gene for vascular endothelial growth factor. Genomic
RT   structure, definition of the transcriptional unit, and
RT   characterization of transcription and post-transcriptional
RT   regulatory sequences.";
RL   J. Biol. Chem. 271:3067-3083(1996).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: VEGF-121 AND VEGF-189 ARE SECRETED, WHILE
CC       VEGF-165 REMAINS CELL-SURFACE-ASSOCIATED UNLESS RELEASED BY
CC       HEPARIN.
CC   -!- ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-121, VEGF-165 AND VEGF-189)
CC       ARE KNOWN AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE
CC       SHORTEST FORM (VEGF-121) DOES NOT BIND HEPARIN, IT MAINLY A FREE
CC       DIFFUSIBLE FACTOR, WHEREAS LONGER FORMS BIND HEPARIN WITH
CC       INCREASING AFFINITY.
CC   -!- TISSUE SPECIFICITY: IN ADULT LUNG EMBRYO, EXPRESSED MAINLY IN
CC       THE ENDOTHELIAL CELLS, LARGE ARTERIES, CAPILLARIES, PLACENTA AND
CC       KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL
CC       GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF
CC       VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ----------
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; S47052; AAB22252.1; -.
DR   EMBL; S48083; AAB22253.1; -.
DR   EMBL; S48160; AAB22254.1; -.
DR   EMBL; M95200; AAA40647.1; -.
DR   EMBL; U41383; -; NOT_ANNOTATED_CDS.
DR   PIR; A43351; A43351.
DR   BSSP; P15692; 2VGH.
DR   MGD; MGI:103178; Vegf.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001620; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    214       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID      51     93       BY SIMILARITY.
FT   DISULFID      82    127       BY SIMILARITY.
FT   DISULFID      86    129       BY SIMILARITY.
FT   DISULFID      76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID      85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     100    100       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC     146    146       K -> N (IN ISOFORM VEGF-120).
FT   VARSPLIC     141    164       MISSING (IN ISOFORM VEGF-164).
FT   VARSPLIC     141    208       MISSING (IN ISOFORM VEGF-188).
FT   CONFLICT     117    118       GE -> EK (IN REF. 2).
SQ   SEQUENCE   214 AA;  25283 MW;  B554085IE4BB6E17 CRC64;

  Query Match             7.4%;  Score 174.5;  DB 1;  Length 214;
  Best Local Similarity  24.0%;  Pred. No. 6.9e-07;
  Matches   47;  Conservative   44;  Mismatches   77;  Indels   ...;  Gaps    ...

Qy      110 EIEKSIQIISGKRKKELKLGHEEKLEGAIVNIEEKFDQVSIYDNSRGELIGSVKNQ 169
            ||:|:||:|:::  ||  ||:||:        ||:||:|:|||||:|:||
Db       38 EVVKEMDVYQRSFCKPIETLVDIFQEYPDEIEYIFKPSCVPLMRCAGCCNDEALEC 97

Qy      170 STNYISKLEAWVTVI-----SDGRLKVEHKNGETRDLVISECKTKSTELRHVQSIV 224
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```
                 |  :  |:   :  |     |  :  :  :||  |:  | |  |  |  :     :|
Db      97 SRSNFTMQIMMIK   PHQGQHIGEMSFLQHSKCECRPKKDRARQENPCGPCSERRKHLFVQDPQTCKCSCKNTDSRCKARQLELNERTCRC 196

                                                                          :
Qy     226     PSEPATQLQCHVANKDCPKNHVWNNQLCRCLAQHDPGFSSHLGDSDIS 272
               :   |   ::      |  : | |:|  :          :|:|      |
Db     154 RKFCPEPKSWCVRCRESRPKKHLFVQDPQTCKCSCKNTDSRCKARQLELNERTCRC 210

                                                                          :
Qy     273 K EEDEEEDQC 282
           : |||: |||
Db     211 QLEENERTCRC 221


RESULT  10
VEGF_CHICK
ID   VEGF_CHICK     STANDARD;      PRT;   216 AA.
AC   P52822; Q01129;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Gallus gallus (Chicken), and
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Chicken; TISSUE=Heart;
RA   Takahashi T.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.c.japonica; TISSUE=Embryo;
RX   MEDLINE=96097892; PubMed=7556923;
RA   Flamme I., von Reutern M., Drexler H.C., Syed Ali S., Risau W.;
RT   "Overexpression of vascular endothelial growth factor in the avian
RT   embryo induces hypervascularization and increased vascular
RT   permeability without alterations of embryonic pattern formation.";
RL   Dev. Biol. 171:399-414(1995).
RN   [3]
RP   SEQUENCE OF 60-187 FROM N.A.
RC   SPECIES=C.c.japonica;
RX   MEDLINE=96011109; PubMed=7781909;
RA   Flamme I., Breier G., Risau W.;
RT   "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT   (flk-1) are expressed during vasculogenesis and vascular
RT   differentiation in the quail embryo.";
RL   Dev. Biol. 169:699-712(1995).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, ENDOTHELIAL
CC       CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS (VEGF 190, VEGF 216 AND VEGF
CC       166) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME
CC       GENE. THE LONGER FORM CONTAINS A BASIC INSERT WHICH ACTS AS A CELL
CC       RETENTION SIGNAL.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY AND EQUALLY EXPRESSED IN HEART AND
CC       LIVER. IN KIDNEY GLOMERULI, BRAIN AND YOLK SAC, VEGF 166 FORM IS
CC       5- TO 10- TIMES MORE ABUNDANT THAN THE VEGF 190 FORM.
CC   -!- DEVELOPMENTAL STAGE: THE VEGF 166 FORM IS EXPRESSED EARLY AT DAY 1
CC       AND IS RIGOROUSLY DURING GASTRULATION. EXPRESSION OF THE VEGF 190
CC       FORM IS DETECTABLE ONLY FROM DAY 2.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; AB011878; BAA24925.1;  -.
DR   EMBL; S79680; AAB35871.1; -.
DR   HSSP; P15692; 2VGH.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    216       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     84    129       BY SIMILARITY.
FT   DISULFID     87    130       BY SIMILARITY.
FT   DISULFID     72     72       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     86     86       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    101    101       N-LINKED (GlcNAc...) (POTENTIAL).
FT   VARSPLIC    112    134       K    N (IN ISOFORM VEGF 166).
FT   VARSPLIC    113    196       MISSING (IN ISOFORM VEGF 166).
FT   VARSPLIC    166    166       E    K (IN ISOFORM VEGF 146).
FT   VARSPLIC    167    210       MISSING (IN ISOFORM VEGF 146).
SQ   SEQUENCE   216 AA;  25203 MW;  82E6C9C2F9FC9DA7 CRC64;


  Query Match              7.2%;  Score 169;  DB 1;  Length 216;
  Best Local Similarity   30.5%;  Pred. No. 1.7e-06;
  Matches   52;  Conservative   47;  Mismatches   77;  Indels   88;  Gaps   10;

Qy      99 PISTEIQKLKEAVAHLKPQGQRATLSKILKAGMTTLEVMSQVVQGGKSPPQLAFNIFTKHFCVSI 158
           : : : :||    |     ::|:|              ||: :::       |:| |: :
El      41 EEEFNEVIKELEV YEESTKFPHIC            LVGSPQIPVEERVSVADITIDGSGNVPI 96

Qy     159 YKQYFYDTKCETSCKKPNRETIHIECSDGSLVPLHNVEHKCSCMSK 204
           :|:|||  |||||: :          :: :|: ::    |  : :  :||  |: | |  |
Db      97 HKQSVVIPAECAHITKVIVPLDGCGKHRKECVAFQEENETLVEQGE 142

Qy     205 LDVYRSVSTIRPQLPATQPQCHVANKPTPKNHVWNNQLCRCLAQHDPGFSSHLGDSDIS 264
           || :    :|     |  :     :  | :
Db     143 KDVKNWVSKIRCPLPKCDRDGLEKHPAPFHLCKEDGQCAYKFHLPTMLEAKQACSEDRAF 202

Qy     265 EEDEEEDQC 273
           | :|  |:|
Db     203 ELNERTCRC 211


RESULT  11
VEGB_MOUSE
ID   VEGB_MOUSE     STANDARD;      PRT;   190 AA.
AC   P49766;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
DE   ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN   VEGFB OR VRF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=96197355; PubMed=8637916;
RA   Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA   Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.;
RT   "Vascular endothelial growth factor B, a novel growth factor for
RT   endothelial cells.";
```

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RL   Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96183052; PubMed=8637968;
RA   Jowusun S., Lagercrantz J., Grimmond S., Silins G.,
RA   Nordenskjvold M., Weber G., Hayward N.K.;
RT   "Characterization of the murine VEGF-related factor gene.";
RL   Biochem. Biophys. Res. Commun. 220:922-928(1996).
CC   -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED. CAN ALSO FORM HETERODIMER
CC       WITH VEGF.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
CC       AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; U43368; AAB06274.1; -.
DR   EMBL; U43369; AAA91493.1; -.
DR   HSSP; P15692; 2VGH.
DR   MGD; MGI:106199; Vegfb.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Signal; Heparin binding.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    188       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   188 AA;  21442 MW;  D52A055EB995E9CA CRC64;
```

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  Query Match             7.0%;  Score 164.5;  DB 1;  Length 188;
  Best Local Similarity  26.0%;  Pred. No. 3.4e-06;
  Matches   50;  Conservative   25;  Mismatches   78;  Indels   55;  Gaps    7;

Qy     107 KFPAAHVNAAFKVSMKLWEFQLTMHFLVCVLVGRELQAGNPEAEGPVHEQLGYDRKMDELESVLNYSGTKGLMRGLRRQQVHSFSHPFQIFHFSFQELTSIMKEIIKFDKRIKNNGNGTWEVEVLTELKKLESEVNHVFLPKDCCQSRKQHKGAGLARPHRPLPSSRPASDPLPMSTVLALPELCQAGNGSSEPLNILDVRVRSVAVTQSRSKSIPIEEYADRIFKNNTKSIKEAIRIQGIQGGTATYKSLVFNTEKKSCSVEEMYKEDSQLTSKSQEEIGKCGREAERWYFDVTAVNQFVRHLGILSEAQCTKENLEFRIGRLETRSNCKLNEDLHVDSGSTPVSPQEFSVRVWSDHQEKPHKEELAPVSVKLSLELEDDSSEAMDNNSHSTSQWLFPLEASLSDVEGLELVHCEKPLFRDQVPHKDFVTLGSHGIVQPSSLQGQNSRWCSQLRSAHSDDSDILIPYDSRHDSVKEVAVGVVCRYPQSHHVNRTVETVTLPLSSLSLPATLIPECEVACGNIHIGFKNPDMDVTFQALIRSRQLNDQLFHVDLLGKPFPGMKDLRPPTPAGQTLILASWDQQSCEGLKKDSDFLRHETMPSAPKNLSMSVNMATRHSQNGTSSKHLREYRMDSQTVSPQSSKHEDDYIMTPVSEFDHVPDYGYKSTLRTAAAVSPTLRTEMEMVTLHLEPTGELDSDLEASFFDSLASDCKMDYKDDDDK
Db      25 QFPVSFSHLFQVVMKLWEFQLTLHFLVCVLVGRELQAGNPEAEGPVHEQLGYDRKMDELESVLNYSGTKGLMRGLRRQQVHSFSHPFQIFHFSFQELTSIMKEIIKFDKRIKNNGNGTWEVEVLTELKKLESEVNHVFLPKDCCQSRKQHKGAGLARPHRPLPSSRPASDPLPMSTVLALPELCQAGNGSSEPLNILDVRVRSVAVTQSRSKSIPIEEYADRIFKNNTKSIKEAIRIQGIQGGTATYKSLVFNTEKKSCSVEEMYKEDSQLTSKSQEEIGKCGREAERWYFDVTAVNQFVRHLGILSEAQCTKENLEFRIGRLETRSNCKLNEDLHVDSGSTPVSPQEFSVRVWSDHQEKPHKEELAPVSVKLSLELEDDSSEAMDNNSHSTSQWLFPLEASLSDVEGLELVHCEKPLFRDQVPHKDFVTLGSHGIVQPSSLQGQNSRWCSQLRSAHSDDSDILIPYDSRHDSVKEVAVGVVCRYPQSHHVNRTVETVTLPLSSLSLPATLIPECEVACGNIHIGFKNPDMDVTFQALIRSRQLNDQLFHVDLLGKPFPGMKDLRPPTPAGQTLILASWDQQSCEGLKKDSDFLRHETMPSAPKNLSMSVNMATRHSQNGTSSKHLREYRMDSQTVSPQSSKHEDDYIMTPVSEFDHVPDYGYKSTLRTAAAVSPTLRTEMEMVTLHLEPTGELDSDLEASFFDSLASDCKMDYKDDDDK 188
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RESULT 12
VEGB_HUMAN
ID   VEGB_HUMAN     STANDARD;      PRT;   188 AA.
AC   P49765;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-AUG-2000 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
DE   FACTOR).
GN   VEGFB OR VRF.
```

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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97027124; PubMed=8919691;
RA   Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S.,
RA   Pravenec M., Braga V., Collins F., Cabrera H., Rakar S., Nordenskjvold M., Ward L.,
RA   Hayward N., Weber G.;
RT   "Cloning and characterization of a novel human gene related to
RT   vascular endothelial growth factor.";
RL   Genome Res. 6:124-131(1996).
CC   -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE LINKED. CAN ALSO FORM HETERODIMER
CC       WITH VEGF.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC       HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; U43368; AAB06274.1; -.
DR   EMBL; U43369; AAA91493.1; -.
DR   HSSP; P15692; 1VPF.
DR   MIM; 601398; -.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50278; PDGF_2; 1.
KW   Mitogen; Growth factor; Signal; Heparin binding.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    188       VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ   SEQUENCE   188 AA;  21261 MW;  F04654D9A4727194 CRC64;
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  Query Match             6.9%;  Score 162.5;  DB 1;  Length 188;
  Best Local Similarity  21.6%;  Pred. No. 4.8e-06;
  Matches   50;  Conservative   26;  Mismatches   80;  Indels   75;  Gaps    7;

Qy     110 AAHVNAAFKVSMKLWEFQLTMHFLVCVLVGRELQAGNPEAEGPVHEQLGYDRKMDELESVLNYSGTKGLMRGLRRQQVHSFSHPFQIFHFSFQELTSIMKEIIKFDKRIKNNGNGTWEVEVLTELKKLESEVNHVFLPKDCCQSRKQHKGAGLARPHRPLPSSRPASDPLPMSTVLALPELCQAGNGSSEPLNILDVRVRSVAVTQSRSKSIPIEEYADRIFKNNTKSIKEAIRIQGIQGGTATYKSLVFNTEKKSCSVEEMYKEDSQLTSKSQEEIGKCGREAERWYFDVTAVNQFVRHLGILSEAQCTKENLEFRIGRLETRSNCKLNEDLHVDSGSTPVSPQEFSVRVWSDHQEKPHKEELAPVSVKLSLELEDDSSEAMDNNSHSTSQWLFPLEASLSDVEGLELVHCEKPLFRDQVPHKDFVTLGSHGIVQPSSLQGQNSRWCSQLRSAHSDDSDILIPYDSRHDSVKEVAVGVVCRYPQSHHVNRTVETVTLPLSSLSLPATLIPECEVACGNIHIGFKNPDMDVTFQALIRSRQLNDQLFHVDLLGKPFPGMKDLRPPTPAGQTLILASWDQQSCEGLKKDSDFLRHETMPSAPKNLSMSVNMATRHSQNGTSSKHLREYRMDSQTVSPQSSKHEDDYIMTPVSEFDHVPDYGYKSTLRTAAAVSPTLRTEMEMVTLHLEPTGELDSDLEASFFDSLASDCKMDYKDDDDK 188
Db      28 APGHQRKVVSWIDVYTRATCQPRELVVVFLIVELMGIVAKQLVPSVVTVQQGCCPDDIT 86

Qy     170 LQCMNTSINYISKILFETVFLCHGRKEVTVCGTANHESCRCMSKEDVYRQVHSILTRRSLP 229
           ||:|: :  :  : | | |  :  :|  |:| | |    :  : | :
Db      87 LECVETCQHQVFMQLIMDYYISPLDLE  MSLEEHSQCECVPPK     EELSAVEFHSF 138

Qy     230 AVSLLSCHVANEFTFKNDVWNNQLFVSLAIDTFEHLGRESTRLMRASIQEPLTFVRAHT 289
                                ||          || ||
Db     139 ---       RPLCP-  -  -  - RC TQH      -  -  -  -                 148

Qy     290 -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  -  - 340
                                  |:  |  :|:| |: :      |   |  : : :|
Db     149 --------- -------HQKPDPRTCRCRCKRRSFLRVQGRGLELNPDTCRC 188
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RESULT  13
VEGF_SHEEP
ID   VEGF_SHEEP     STANDARD;      PRT:  146 AA.
AC   P50411;
DT   01-OCT-1995 (Rel. 34, Created)
DT   01-OCT-1995 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE   PERMEABILITY FACTOR) (VPF).
GN   VEGF.
OS   Ovis aries (sheep)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97117956; PubMed=8990012;
RA   Redmer D.A., Doraiswamy V., Bortnem B.J., Viglianti J.A.,
RA   Reynolds L.P., Morrow K.M.;
RT   "Characterization and expression of vascular endothelial growth
RT   factor (VEGF) in the ovine corpus luteum.";
RL   J. Reprod. Fertil. 106:157-165(1996).
CC   -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC       CELL GROWTH, INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC       PERMEABILITY.
CC   -!- SUBUNIT: HOMODIMER, DISULFIDE LINKED.
CC   -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC       TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X96506; CAA65277.1; -.
DR   HSSP; P15692; 1VPF.
DR   InterPro; IPR000072; PDGF.
DR   Pfam; PF00341; PDGF; 1.
DR   ProDom; PD001629; PDGF; 1.
DR   SMART; SM00141; PDGF; 1.
DR   PROSITE; PS00249; PDGF_1; 1.
DR   PROSITE; PS50270; PDGF_2; 1.
KW   Mitogen; Growth factor; Glycoprotein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    146       VASCULAR ENDOTHELIAL GROWTH FACTOR.
FT   DISULFID     51    ?         BY SIMILARITY.
FT   DISULFID     60    127       BY SIMILARITY.
FT   DISULFID     86    129       BY SIMILARITY.
FT   DISULFID     76     76       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     85     85       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   146 AA;  17247 MW;  4E7962B05/E9176D0 CRC64;

  Query Match             4.7%;  Score 1080.5;  DB 1;  Length  146;
  Best Local Similarity   33.0%;  Pred. No. 7.7e-66;
  Matches   96;  Conservative   18;  Mismatches   32;  Indels    0;  Gaps    3;

Qy      116 EIEKSIDIFDKRKRVQMDPEVVVRLKKEIGALTNIEFKFEPPCVSLVRCTGCCNNEGLE 175
            ||:|| :| :::   | |  || :|:        ||| || : ||||||| | |||
Db       48 EVMKEMDVYQRSFCQDVEIESGEYPDEIEFIFKPSCVPLMRCGGCCNDEGLE   99

Qy      176 CVPTSEKSNITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRAR 221
                :    | |||  :    |  : :  :|| | | |  | |  :|
Db       98 CACRPKKDR   146
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Db      94      VEIEEENITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRAR 140

RESULT  14
EBNI_MOUSE
ID   EBNI_MOUSE     STANDARD;      PRT:  2871 AA.
AC   Q61571; Q60826;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   FIBRILLIN 1 PRECURSOR.
GN   EBNI OR FBN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95130561; PubMed=7829516;
RA   Yin W., Gerhiller J., Sanquinetti C., Smiley E., Pangilinan T.,
RA   Pereira L., Ramirez F., Bonadio J.;
RT   "Primary structure and developmental expression of Fbn-1, the mouse
RT   fibrillin gene.";
RL   J. Biol. Chem. 270:1208-1216(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL; TISSUE=Kidney;
RA   Ota K., Kumar A., Wada J., Lin Z., Kanwar Y.S.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FBN-1 IS A STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC       THAT BINDS CALCIUM. FIBRILLIN 1 CONTAINING MICROFIBRILS PROVIDE
CC       LONG-TERM FORCE-BEARING STRUCTURAL SUPPORT.
CC   -!- FBN1 FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
CC       FIBRILLIN 1 MOLECULES OR WITH OTHER COMPONENTS OF THE
CC       MICROFIBRILS (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM-BINDING
CC       EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 7 TGF-BETA-BINDING PROTEIN DOMAINS.
CC
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; L29454; AAA36846.1; -.
DR   EMBL; U22493; AAA64217.1; -.
DR   HSSP; P35555; 1AP0.
DR   MGD; MGI:95489; Fbn1.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF_like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR002212; TB.
DR   Pfam; PF00008; EGF; 46.
DR   Pfam; PF00683; TB; 9.
DR   SMART; SM00179; EGF_CA; 42.
DR   SMART; SM00181; EGF_like; 4.
DR   PROSITE; PS00010; ASX_HYDROXYL; 43.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 98.
DR   PROSITE; PS01187; EGF_CA; 45.
KW   Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW   Repeat; Signal; Multigene family.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28   2871       FIBRILLIN 1.
FT   DOMAIN       81    112       EGF-LIKE 1; NON-CALCIUM-BINDING.
FT   DOMAIN      115    146       EGF-LIKE 2; NON-CALCIUM-BINDING.
FT   DOMAIN      147    178       EGF-LIKE 3; NON-CALCIUM-BINDING.
FT   DOMAIN      246    287       EGF-LIKE 4; CALCIUM-BINDING.
FT   DOMAIN      288    329       EGF-LIKE 5; CALCIUM-BINDING.
FT   DOMAIN      330    461       TGFBP 1.
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FT   DOMAIN      402    446       PRO RICH.
FT   DOMAIN      449    489       EGF LIKE 6, NON CALCIUM BINDING.
FT   DOMAIN      490    529       EGF LIKE 7, CALCIUM BINDING.
FT   DOMAIN      530    571       EGF LIKE 8, CALCIUM BINDING.
FT   DOMAIN      572    612       EGF LIKE 9, CALCIUM BINDING.
FT   DOMAIN      613    653       EGF LIKE 10, CALCIUM BINDING.
FT   DOMAIN      656    721       TGFBP 2.
FT   DOMAIN      723    764       EGF LIKE 11, CALCIUM BINDING.
FT   DOMAIN      765    806       EGF LIKE 12, CALCIUM BINDING.
FT   DOMAIN      807    846       EGF-LIKE 13, CALCIUM BINDING.
FT   DOMAIN      910    951       EGF LIKE 14, CALCIUM BINDING.
FT   DOMAIN      952   1018       TGFBP 3.
FT   DOMAIN     1028   1069       EGF LIKE 15, CALCIUM BINDING.
FT   DOMAIN     1070   1112       EGF LIKE 16, CALCIUM BINDING.
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FT   DOMAIN     1155   1196       EGF LIKE 18, CALCIUM BINDING.
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FT   DOMAIN     1487   1527       EGF LIKE 26, CALCIUM BINDING.
FT   DOMAIN     1528   1599       TGFBP 4.
FT   DOMAIN     1606   1647       EGF LIKE 27, CALCIUM BINDING.
FT   DOMAIN     1648   1688       EGF-LIKE 28, CALCIUM BINDING.
FT   DOMAIN     1693   1758       TGFBP 5.
FT   DOMAIN     1765   1807       EGF LIKE 29, CALCIUM-BINDING.
FT   DOMAIN     1808   1848       EGF LIKE 30, CALCIUM BINDING.
FT   DOMAIN     1849   1890       EGF LIKE 31, CALCIUM BINDING.
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FT   DOMAIN     1933   1972       EGF LIKE 33, CALCIUM BINDING.
FT   DOMAIN     1973   2012       EGF LIKE 34, CALCIUM BINDING.
FT   DOMAIN     2013   2054       EGF LIKE 35, CALCIUM BINDING.
FT   DOMAIN     2055   2121       TGFBP 6.
FT   DOMAIN     2127   2165       EGF LIKE 36, CALCIUM BINDING.
FT   DOMAIN     2166   2205       EGF LIKE 37, CALCIUM BINDING.
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FT   DOMAIN     2291   2332       EGF LIKE 40, CALCIUM BINDING.
FT   DOMAIN     2333   2401       TGFBP 7.
FT   DOMAIN     2402   2443       EGF LIKE 41, CALCIUM BINDING.
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  Query Match             6.5%;  Score 152;  DB 1;  Length 2871;
  Best Local Similarity   25.2%;  Pred. No. 0.00053;
  Matches   79;  Conservative   27;  Mismatches  111;  Indels   96;  Gaps   21;

Qy        155 CVCIYRC   [illegible]CMNICINYIGKILFEIIVPLSHCPKPVIVCPANHISCKCM 211
              |:    |     | |   |   :|:|         ||    |    :  |         |:  |   |:
Db       2289 CIDENECQIKRGIC   ENGRCLN          ILGSYICECNEG      FIACEIQDECL 2332

Qy        212 SKLDVY          RQVHSIIRRSLFAIQIQCHVANKICPKNHVW   NNQI[illegible]        253
                :  |          |:  :   |    | |:::|       |       |   : :|
Db       2333 DNRKGYCTSEVFENMCQIGSSNRN  IVIKSEC     CCVG[illegible]RGWGLDPELICPEEGIVA 238[illegible]

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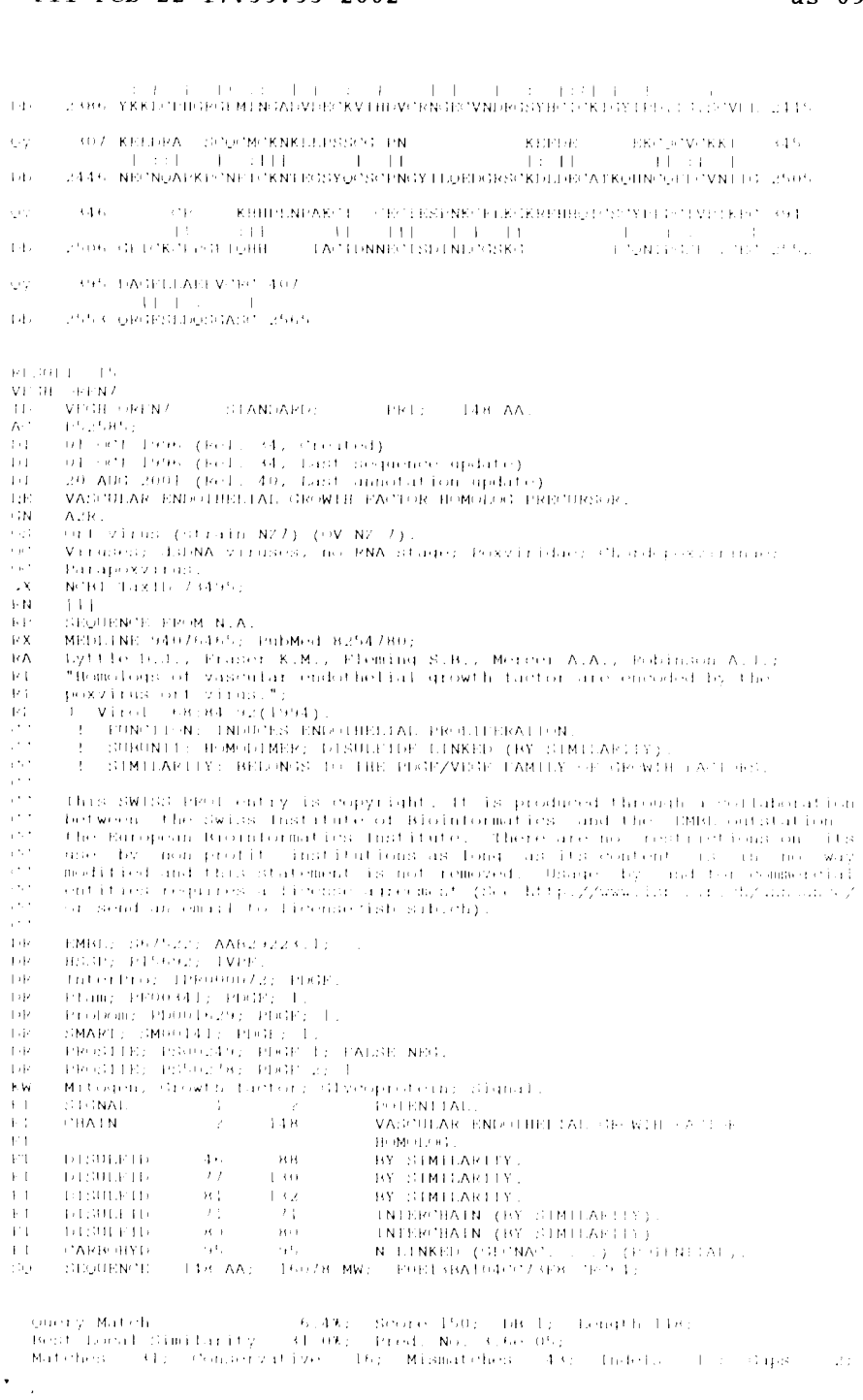


Search completed: February 20, 2002, 16:27:33
Job time: 171 secs

M.p.Prot: protein search, using sw model

Run on: February 20, 2002, 10:20:18 ; Search time: 2.00 Seconds
(without alignments)
124.750 Million cell updates/sec

Title: US-09-534-376A-13
Perfect score: 2854
Sequence: 1 MRLLEMDSLSGVLAAVMLVTLQAAEVVKGVRLGKHVGCYGN 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 75174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

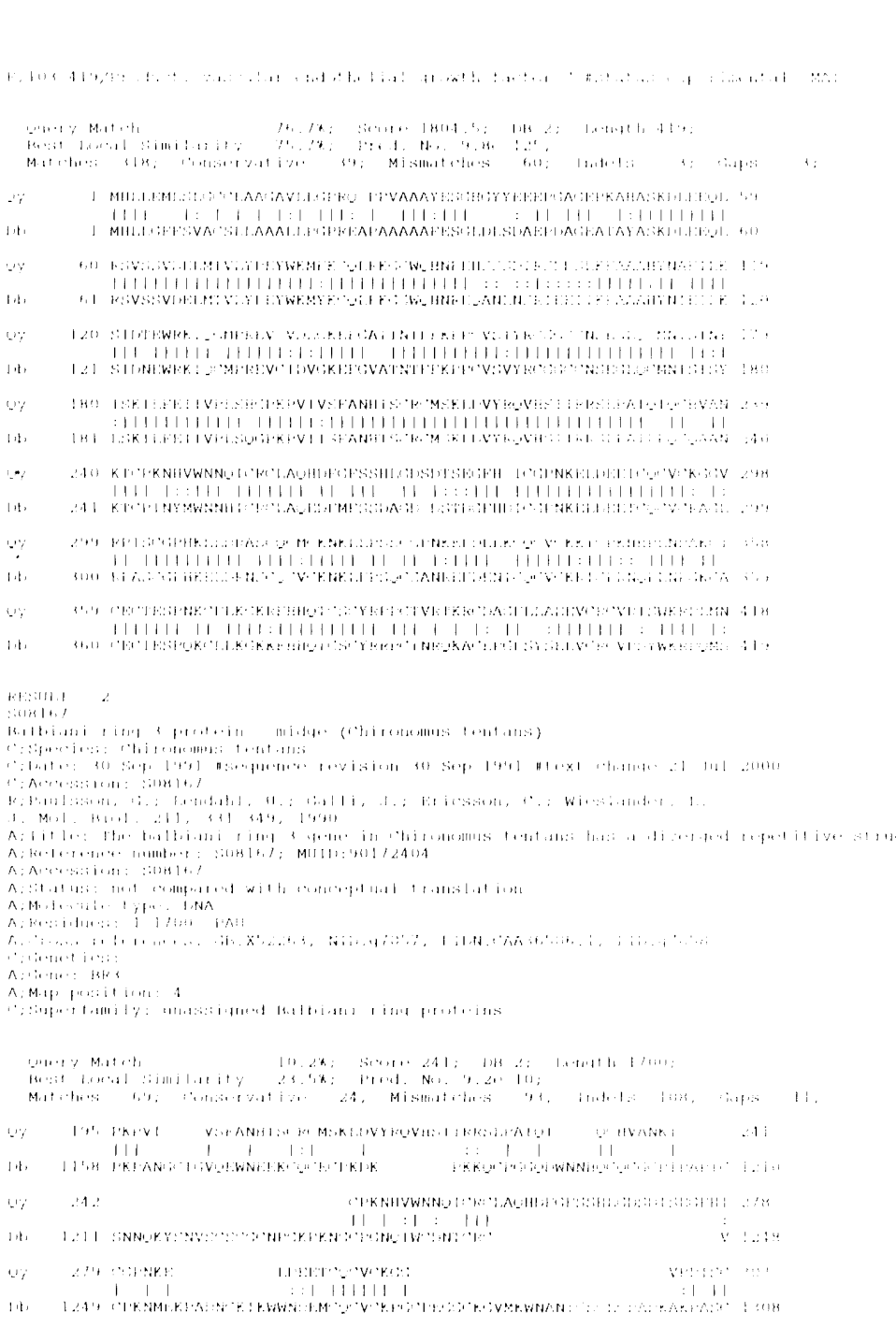
Qy, N, is the number of results produced by that query, i.e. a score greater than or equal to the score of the result in that position, and is derived by analysis of the total score distribution.

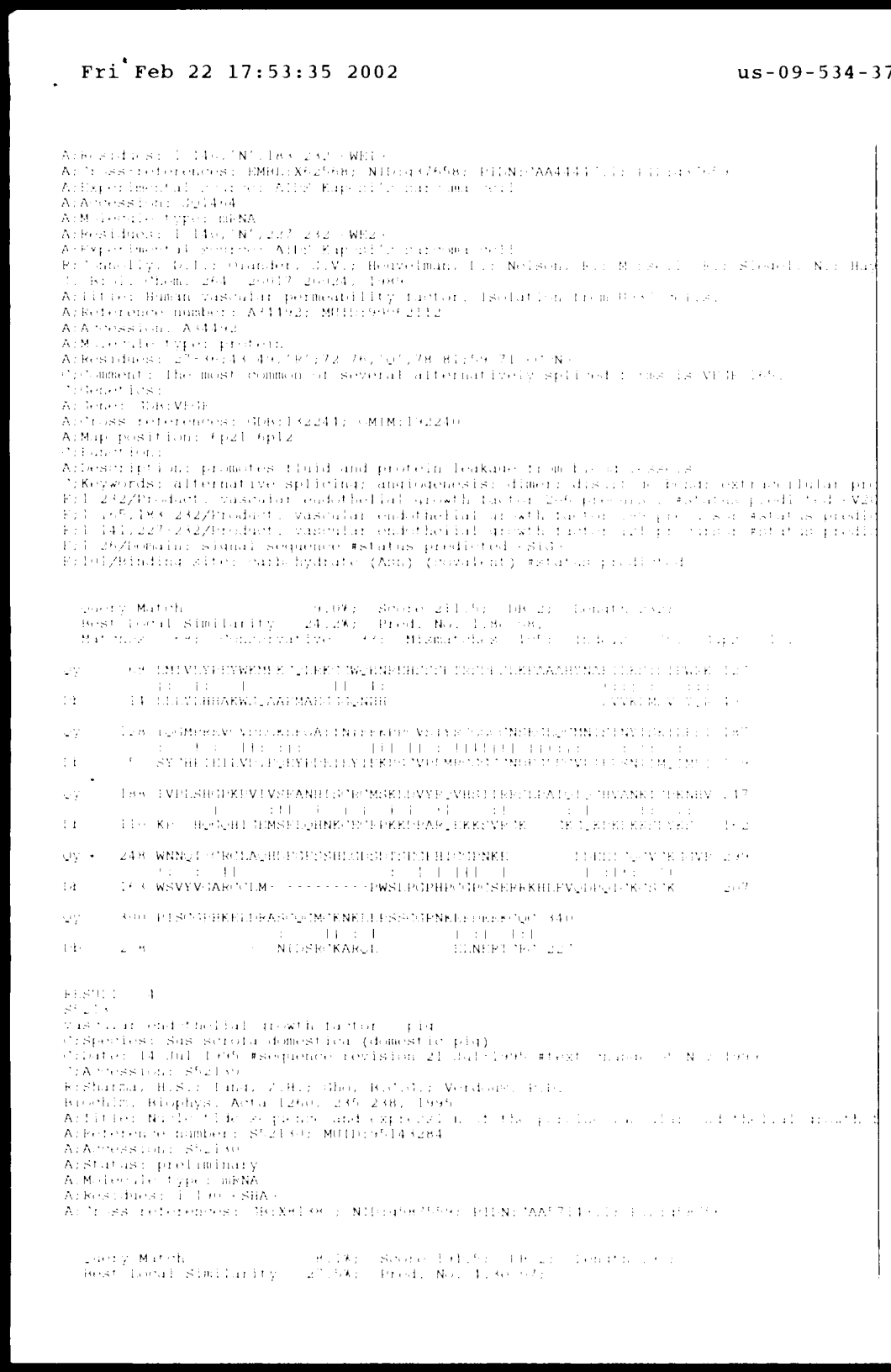
SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1845.5	64.7	419	2	S69207	vascular endothelial
2	241	8.4	1705	2	S96267	Bacillus subtilis pr
3	211.5	7.4	232	2	A41551	vascular endothelial
4	191.5	6.7	196	2	S52150	vascular endothelial
5	189.5	6.6	196	2	B44881	vascular endothelial
6	188.5	6.6	196	2	A35987	alfalfa derived vas
7	179.5	6.3	190	2	B40080	vascular endothelial
8	174.5	6.1	214	2	A44881	vascular endothelial
9	174	6.1	160	2	JQ0542	18K secretory pro
10	170.5	6.0	1187	2	I18356	hypothetical pr te
11	164.5	5.8	188	2	JC4680	vascular endothelial
12	158.5	5.6	146	2	S57956	zinc-vascular endo
13	157.5	5.5	120	2	A43787	vascular endothelial
14	152	5.3	2871	2	A56624	tigrillin 1 precur
15	150	5.3	148	2	D49530	18K vascular endot
16	144	5.1	3082	2	A47221	tigrillin 1 precur
17	143.5	5.0	133	2	B49580	vascular endotheli
18	141.5	5.0	4712	2	S18253	laminin alpha 2 ch
19	141	4.9	149	2	A41236	proteoglycan 4-with t
20	141	4.9	1111	2	I25922	hypothetical pr te
21	140	4.9	1077	2	I41145	protein tyrosine
22	140	4.9	2871	2	A56623	tigrillin 2 - huma
23	138.5	4.9	1810	1	A42280	fibrinogen precursor
24	138	4.8	837	2	A42112	P-rich like peptide
25	137.5	4.8	1104	2	I48869	transcription fac
26	137.5	4.8	1203	2	A49175	Notch 3 protein
27	137.5	4.8	1964	2	I09659	notch1 - mouse
28	137	4.8	207	2	JC4679	vascular endothelial
29	136.5	4.8	473	2	A56125	adhesive protein pr
30	135	4.7	2150	2	I42497	hypothetical prote
31	135	4.7	2318	2	S45389	notch 3 protein
32	134.5	4.7	2201	2	A52164	tenascin C - human
33	134	4.7	1872	2	I25933	hypothetical pr te
34	134	4.7	2703	1	A24420	1-195 protein - ra
35	133.5	4.7	861	2	I10514	Not 1 protein pr tei
36	133	4.6	2321	2	S78543	1-2-23 protein - h
37	132	4.6	128	2	I51295	vascular endothelial
38	132	4.6	1034	2	JC6508	mucin - rat
39	132	4.6	1296	2	I16859	hypothetical prote
40	131.5	4.6	2531	2	A46019	Notch 1 protein
41	131	4.6	158	2	A56125	placental growth f
42	130	4.5	647	2	A43902	tenascin - rabbit
43	130	4.5	1220	2	A56159	fibrinogen protein pro
44	129.5	4.5	1109	2	I15408	gene shuttle protein
45	129.5	4.5	1109	2	I44598	hypothetical pr te

ALIGNMENTS

RESULT 1
S69207
vascular endothelial growth factor C precursor - human
N;Alternate names: FLT4 ligand BBM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C;Accession: S69207; S61795; S71443; S69208; G02659
R;Joukow, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A;Reference number: S69207; MUID:96203004
A;Accession: S69207
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <JOU>
A;Cross-references: EMBL:X94216; NID:g1174486; PIDN:CAA64217.1; PID:g22007; GI:1178
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 199
A;Note: only a part of the translation is shown
A;Note: this is a revision to the sequence from reference S61795
R;Joukow, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksel
EMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4
A;Reference number: S61795; MUID:96178224
A;Accession: S61795
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 7-419 <JOU>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
A;Molecule type: protein
A;Residues: 'X',104-120 <JOU2>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and
A;Reference number: S69208
A;Accession: S69208
A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150088; PIDN:AAA85214.1; PID:g1150089
R;Morris, J.C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01557
A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
A;Cross-references: EMBL:U58111; NID:g1473426; PIDN:AAB02966.1; PID:g1473427
C;Genetics:
A;Gene: GDB:VEGFC; VRP
A;Cross-references: GDB:389088; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>





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Matches 49; Conservative 40; Mismatches 66; Indels 51; Gaps 4;

RESULT 5
B44801
vascular endothelial growth factor 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Nov-1994
C;Accession: B44801; A43851; A45619
R;Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.
Development 114, 521-532, 1992
A;Title: Expression of vascular endothelial growth factor during embryonic angiogenesis
A;Reference number: A11981; MEDLINE;92234860
A;Accession: B44801
A;Molecule type: mRNA
A;Residues: 1-190 <BRE>
A;Cross-references: BerSeq0083; NID:g240858; PIDN:AAB22255.1; PID:g240859
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:139122, NCBIP:139123)
R;Plouet, J.; Moukadiri, H.; Gospodarowicz, D.
J. Biol. Chem. 264, 18511-18514, 1989
A;Title: Vascular endothelial growth factor, regulation by cell differentiation and a
A;Reference number: A43951; MEDLINE;90285993
A;Accession: A43951
A;Molecule type: mRNA
A;Residues: 1-116,'EK',119-190 <PLA>
A;Cross-references: GB:M32315; NID:g202350; PIDN:AAA40947.1; PID:g202351
A;Note: sequence extracted from NCBI backbone (NCBIN:139665, NCBIP:139675)
R;Gospodarowicz, D.; Mescher, A.L.; Plouet, J.
Growth Factors 4, 53-59, 1990
A;Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelia
A;Reference number: A45619; MEDLINE;91079943
A;Accession: A45619
A;Molecule type: protein
A;Residues: 27-98 <PUS>
C;Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;

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RESULT 4
S52150
vascular endothelial growth factor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Nov-1995
C;Accession: S52150
R;Sharma, H.S.; Ehara, Z.R.; Olsen, R.C.L.; Verdonk, P.H.
Brochim. Biophys. Acta 1260, 235-238, 1995
A;Title: Neuropeptide Y-like immunoreactivity in the porcine cerebrospinal fluid
A;Reference number: S52150; MUID:95144284
A;Accession: S52150
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <SHA>
A;Cross-references: GB:X81388; NID:g506556; PIDN:CAA57114.1; PID:g506557

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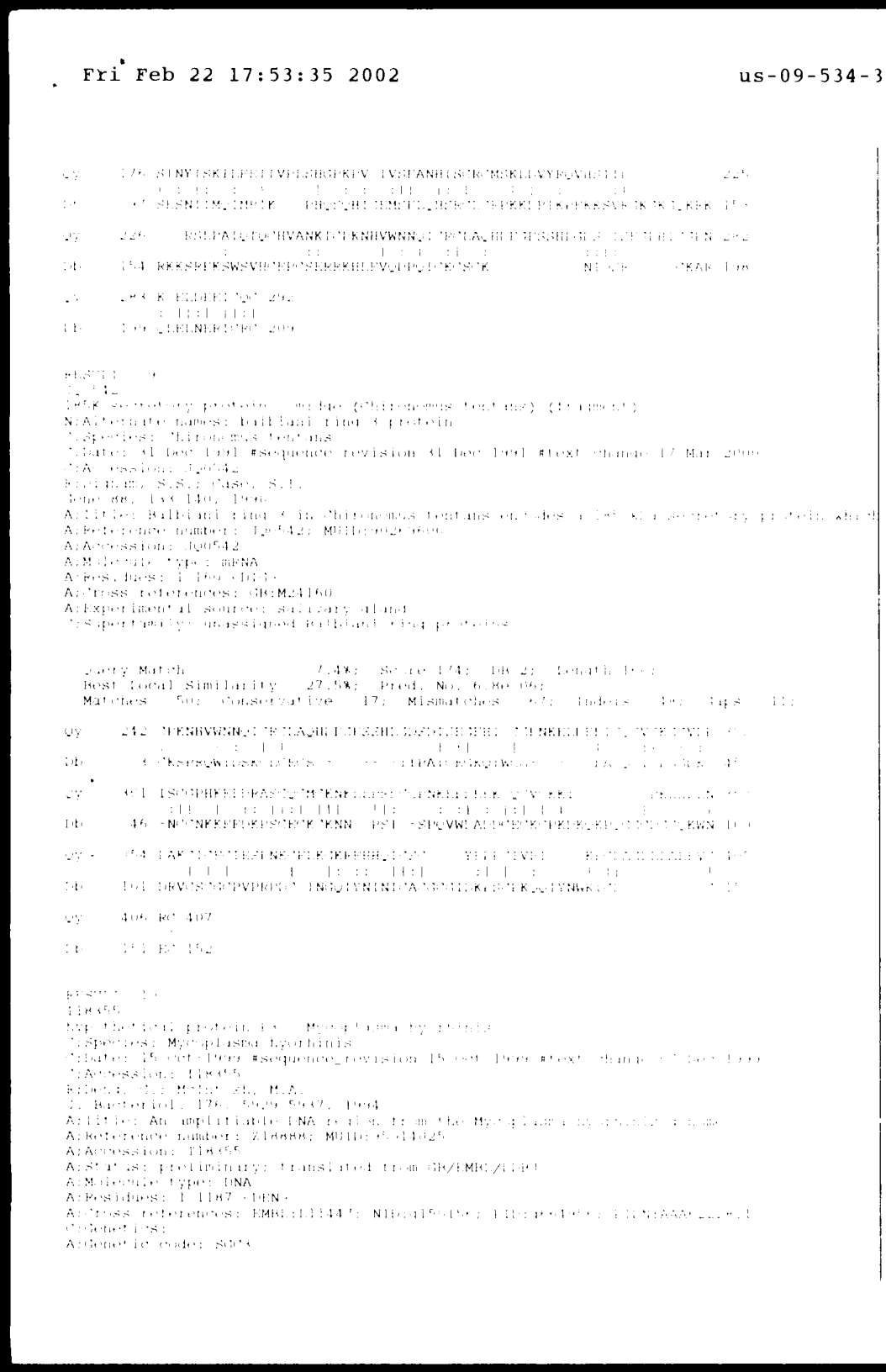

RESULT 11
JC4680
vascular endothelial growth factor related factor 167 precursor - mouse
N;Alternate names: VRF 167 protein
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C;Accession: JC4680
R;Townson, S.; Lauderdale, J.; Grimmond, S.; Stilms, G.; Nordeen, P.; Weber, G
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A;Title: Characterization of the murine VEGF-related factor gene.
A;Reference number: JC4667; MUID:96186052
A;Accession: JC4680
A;Molecule type: mRNA
A;Residues: 1-188 <TOW>
A;Cross-references: GB:U43847; NID:g1314455; PIDN:AAC52753.1; PID:g1314456
C;Comment: This factor is a mitogen, that is selective for endothelial cells, and bel
ar endothelial growth factors 167 and VegF 189.
C;Genetics:
A;Gene: vrf
A;Map position: 19
A;Introns: 137/2
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-188/Product: vascular endothelial growth factor related factor #status pred. <ret

Query Match 7.2%; Score 164.5; DB 2; Length 188;
Best Local Similarity 26.0%; Pred. No. 4e-05;
Matches 50; Conservative 25; Mismatches 78; Indels 39; Gaps 7;

Qy 107 KPAAAHYNAEILKSIPIEPSDPTEWFEILGHPMFVPFDEEHSKAILNLTPPHPDVSGYVEDGVN 166
Db 29 QEIVSTCACIFKPVTRVMVQIGKEPTYNEDFMGSVVPERARPVFSVAVDSWTYVTKKTKDLQKV 88

Qy 167 SEGLQCMNISFNYIQKLYETDVKLLKTESVVHPTRPSYLESDVLYLDHNSNMLANLSVTEHVSIE 226
Db 89 IKGLDYKSCVFVGCPTRVKQGTISRFYFNLSSVRDNIDRLELKLSKSQVEDEAVWFAIDKVSED 148

Qy 227 DCL PCSLTRRHLTVGFSVKANKDTKNHVWNNCITSKCLAQHDDFGFSSHLGSLSFLEDHELSGD 286

Qy 287 PNKELDETCQC 298
Db 149 PGLELNEDTCM 160

RESULT 12
S07956

vascular endothelial growth factor - sheep
C;Species: Ovis aries (sheep), Ovis ammon aries (domestic sheep)
C;Date: 14-Jan-1996 #sequence revision 01-Mar-1996 #text change 09-Nov-1999
C;Accession: S57956
R;Redmer, D.A.; Doll, Y.; Li, J.; Jones, S.C.; Moore, K.M.
Submitted to the EMBL Data Library, July 1995
A;Reference number: S57956
A;Accession: S57956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <RED>
A;Cross-references: EMBL:X89506; NID:g809350; PIDN:CAA62677.1; PID:g809351

Query Match 6.2%; Score 156.5; DB 2; Length 115;
Best Local Similarity 33.0%; Pred. No. 8.5e-05;
Matches 95; Conservative 19; Mismatches 42; Indels 14; Gaps 1;

Qy 116 EELKSIDIEWMKTIGMPREVCVDLGKEFGATFNIPFKMDVVSGYKCIYNCTSVRCM 275
Db 68 EVMKTMDVYSIGSFCKTDCVEPGDITLKFKNMFTPYPEPRASLLENVTQAMG 225

Qy 276 SINYIGKTFFEITVPS SHCGKPRV IVSFANHTSCPPMSKDSVFE 419
Db 94 VFIDIGNEGIM_IMPLKKA_SRTIRMSFLVHKSNLGEIGVE 225

RESULT 13
Z66787
vascular endothelial growth factor (version 1) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Mar-1998 #sequence revision 16-Mar-1998 #text change 09-Nov-1999
C;Accession: A33787
R;Fiscaber, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Shushan, B.; Lau, K.; Tisp
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989
A;Title: Vascular endothelial growth factor: a new member of the platelet derived growth
A;Reference number: A33787; MUID:90128225
A;Accession: A33787
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <FIS>
A;Cross-references: GB:M32795; NID:g189819; PIDN:AAA30905.1; PID:g189820
C;Keywords: alternative splicing

Query Match 6.2%; Score 157.5; DB 2; Length [illegible];
Best Local Similarity 33.0%; Pred. No. 8.6e-05;
Matches 96; Conservative 18; Mismatches 42; Indels 14; Gaps 1;

Qy 116 EELKSIDIEWMKTIGMPREVCVDLGKEFGATFNIPFKMDVVSGYKCIYNCTSVRCMN 276
Db 12 EVVKTMDVYSIGSFCKTDCVEPGDITLKFKNMFTPYPEPRASLLENVTQAMG 69

Qy 276 SINYIGKTFFEITVPS SHCGKPRV IVSFANHTSCPPMSKDSVFE 419
Db 68 VFIDIFPNIIMQIMFIKFHQRQHIDGRMSFLQHNKCECRPKKDKARQ 115

RESULT 14
A56624
fibrillin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence revision 23-Mar-1995 #text change 11-Jan-2000
C;Accession: A56624
R;Yin, W.; Smiley, E.; Germiller, J.; Sakamoto, T.; Eastman, S.; Ferrara, J.; Bartels,
J. Biol. Chem. 270, 17124-17130, 1995
A;Title: Primary structure and developmental expression of fbn-1, the mouse fibrillin ge
A;Reference number: A56624; MUID:95360561
A;Accession: A56624
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: GB:L27454; NID:g575609; PIDN:AAA39943.1; PID:g575611

C;Genetics:
A;Gene: FBN 1
C;Superfamily: unassigned EGF related proteins; EGF homology
F;1201-1236/Domain: EGF homology <EGF>

Query Match 6.5%; Score 152; DB 2; Length 2871;
Best Local Similarity 25.2%; Pred. No. 0.00[illegible];
Matches 79; Conservative 27; Mismatches 111; Indels 99; Gaps 21;

Qy 159 CVSIYRC GGCCNRNRLQEMNTCGYGKFCETRVPDSRPSCKFVKVSLANHTSCMK 211
Db 2289 CTEINECVIKPGIC ENGFCLN IDGSYTCECNDG FIASETLECL 2335

Qy 212 GKEIVY RCVHCTEPRSLPATCTLCVDVANKTFPKNHVW NNCTC 259
Db 2336 EGEECYCFGLVFEENMCYESSNRN FVIKGRC CVSGNCWCLHCEECPFESIVA 2387

Qy 260 PCGADPVVYEVHTNMAQIRTACKDKDMKLWLSHLRNLT SEEIVVERGVRD DSYGFM 439
Db 2388 YKKICTPEDCPDMINCAEVESPKEVIHHVCMGNCPVNCPHQSYWCPKLQYIPCLTCTSVE 2447

Qy 440 KEIIEA CSCVMPKKNKEIIGSVSIPN KEIIE EKCVCVCKKI 485
Db 2448 NGMCWCVNTEGVRRNDSMHISIMKCRIQDCHPDLPYMASFCVVDIKS 2495

Qy 486 CP KHHPLNDAEC CYCIESFNKCPFLSGKRFHHEQTCSCYRPPCTVPLEKC 534
Db 2496 GECKCLPGRFLQHH IACTDNNECISIENLCISKK DCQNTEGSF DCQ 2542

Qy 535 DAGFLIAEEVCKC 547
Db 2543 QKCRSIQSGASC 2555

RESULT 15
D47540
16K vascular endothelial growth factor homolog A2R - orf virus
C;Species: orf virus
C;Date: 07-Apr-1994 #sequence revision 08-Nov-1994 #text change 08-Oct-1999
C;Accession: I47540
R;Ueda, S.; Fraser, K.M.; Plowman, G.D.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o
A;Reference number: A47540; MUID:94076465
A;Contents: N.T.
A;Accession: I47540
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <YIY>
A;Cross-references: GB:S67522; NID:g456000; PIDN:AAB29223.1; PID:g456001
A;Note: sequence extracted from NCBI backbone (NCBIN:143422, NCBIP:143429)

Query Match 6.4%; Score 150; DB 2; Length 148;
Best Local Similarity 31.0%; Pred. No. 9.3e-06;
Matches 91; Conservative 16; Mismatches 43; Indels 14; Gaps 2;

Qy 124 EWRKIGT MEELVVEHGKEPGAIFNITLEKHTCVCRPKRSDTNSFEDLPMNIGNY 179
Db 9 EWMELIDKSGSCKEKDIVVYYGEEYFESLNLQYNFEHCVIVEPCSGCNGDGLQICTAVEIEN 68

Qy 180 IGKLIDEIVPEHCDPKP VIVSFANHTSCPPMPK 213
Db 69 IIVEVSVIDGVSSSSSLENSSVSINLQKISVIEHHIKCDCHGH 109

Search completed: February 20, 2002, 16:26:20
Job time: 52.8 sec

GenCore version 4.5
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SW protein protein search, using sw model

Run on: February 20, 2002, 16:25:45 ; Search time 2.22 Seconds
(without alignments)
2340.894 Million cell updates/sec

Title: US-09-534-376A-13
Perfect score: 2854
Sequence: 1 MRQLHSKDSIVSLAAYVLELDWRDSPAAEIKKLEDEDEGLMVRGQVDVPFVAETGKLSLAY...

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74672298 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Sep01:*
1: geneseq-aa1:*
2: geneseq-aa2:*
3: geneseq-aa3:*
4: geneseq-aa4:*
5: geneseq-aa5:*
6: geneseq-aa6:*
7: geneseq-aa7:*
8: geneseq-aa8:*
9: geneseq-aa9:*
10: geneseq-aa10:*
11: geneseq-aa11:*
12: geneseq-aa12:*
13: geneseq-aa13:*
14: geneseq-aa14:*
15: geneseq-aa15:*
16: geneseq-aa16:*
17: geneseq-aa17:*
18: geneseq-aa18:*
19: geneseq-aa19:*
20: geneseq-aa20:*
21: geneseq-aa21:*
22: geneseq-aa22:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2854	100.0	418	18	AAW00944	Vascular E
2	2854	100.0	418	19	AAW75743	Vascular end
3	1804.5	76.7	419	18	AAW17837	Human E
4	1804.5	76.7	419	18	AAW00942	Human E
5	1804.5	76.7	419	18	AAW75740	Human Vascular
6	1804.5	76.7	419	20	AAW86233	Human Vascular
7	1804.5	76.7	419	21	AAB10049	Human VEGF
8	1804.5	76.7	419	21	AAB29818	Human VEGF
9	1804.5	76.7	419	21	AAY78749	Human
10	1804.5	76.7	419	21	AAY70982	Human Vascular
11	1804.5	76.7	419	22	AAB37605	Human VEGF
12	1795.5	76.5	419	18	AAW18833	Human Vascular
13	1794.5	76.2	419	20	AAY85519	Vascular end
14	1794.5	76.2	419	20	AAY22320	Full length human
15	1794.5	76.2	419	21	AAY97144	Vascular endothelial
16	1794.5	76.2	419	22	AAY97570	Human VEGF R
17	1794.5	76.2	419	19	AAW75761	Vascular endothelial
18	1791.5	76.1	419	18	AAW11478	Human vascular end
19	1750.5	74.7	399	20	AAW86237	Human VEGF fetal
20	1747.5	74.2	415	19	AAW75742	Mouse vascular end
21	1742.5	74.0	419	18	AAW00943	Mouse E24 receptor
22	1604	68.1	450	20	AAY85519	A fragmented vascu
23	1604	68.1	450	20	AAY22421	Truncated human VE
24	1604	68.1	450	21	AAY97145	Truncated vascular
25	1604	68.1	450	22	AAY97577	Human VEGF 2 precu
26	1599	67.9	450	18	AAW82686	Vascular endothelia
27	1453	61.7	438	20	AAY68284	Human growth factor
28	1417	60.2	307	20	AAW86222	Human VEGF 2 truncat
29	1391	59.1	302	20	AAW86223	Human VEGF 2 truncat
30	1370	58.2	297	20	AAW86224	Human VEGF 2 truncat
31	1343	57.1	292	20	AAW86225	Human VEGF 2 truncat
32	677	28.8	425	19	AAW53240	Homo sapiens vascu
33	677	28.8	425	22	AAY97572	Human VEGF 2 pre-pr
34	677	28.8	454	19	AAW49046	Human vascular end
35	677	28.8	454	19	AAW55241	Homo sapiens vascu
36	677	28.8	454	20	AAW44293	Human vascular end
37	677	28.8	454	21	AAB10049	Human VEGF pre-pro
38	677	28.8	454	21	AAB29849	Human VEGF pre-pro
39	677	28.8	454	21	AAY70756	Human prepro vascu
40	677	28.8	454	21	AAY70983	Human vascular end
41	677	28.8	454	22	AAY97573	Human VEGF 21 prot
42	677	28.8	454	22	AAB37606	Human VEGF 1- Hom
43	675	28.7	454	22	AAB70685	Human vascular end
44	669.5	28.5	447	20	AAY68286	Human growth factor
45	668	28.4	454	18	AAW55242	Mus musculus vascu

ALIGNMENTS

RESULT 1
AAW00944
ID AAW00944 standard; protein; 418 AA.
XX
AC AAW00944;
XX
DT 13-NOV-1997 (first entry)
XX
DE Soluble E24 receptor 1, vascular endothelial growth factor.
XX
KW VEGF; E24; receptor; tyrosine kinase; VEGFR; soluble;
KW cardiovascular; vascular; flt4; fetal receptor; ligand;
KW angiogenesis; wound healing; lymph vessel; therapy; diagnosis.
XX
OS Coturnix coturnix.
XX
PN WO9705250-A2.
XX
PD 13-FEB-1997.
XX
PF 01-AUG-1996; 96WO-FI000427.
XX
PR 28-JUN-1996; 96US-0671573.
PR 01-AUG-1995; 95US-0510144.
PR 15-JAN-1996; 96US-0585895.
PR 14-FEB-1996; 96US-0601342.
XX
PA (OYHE) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Joukov V;
XX
DR WPI; 1997-145688/13.
DR N-PSDB; AA18430.
XX

PT FLT4 receptor tyrosine kinase ligand and related nucleic acid used
PT to modulate growth of endothelial cells and for diagnosis of
PT endothelial cell diseases
XX
PS Example 20; Page 126-127; 184pp; English.
XX
CC This polypeptide sequence comprises quail VEGF-C, a novel ligand
CC that binds specifically to the FLT4 receptor tyrosine kinase
CC (VEGFR-3), stimulating phosphorylation of the receptor, and which
CC modulates the growth of endothelial cells. The sequence was
CC deduced from a cDNA clone (AAT84300) obtained from a quail cDNA
CC library, and shows a high degree of homology to novel, claimed
CC human VEGF-C (see AAW00932) and mouse (see AAW00933) VEGF-C.
CC Recombinant quail VEGF-C polypeptides can be produced that
CC correspond to non-human mammalian variants of VEGF-C.
XX
SQ Sequence 418 AA;

Query Match 100.0%; Score 2354; DB 18; Length 418;
Best Local Similarity 100.0%; Prod. No. 2.8e-188;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHLLEMLSTASFCLAAGAVLLGTRQAPVAAAYESGVDYYEIEPQVGEFKAVAKSKDLEEQLR 60
Db 1 MHLTEMLSLPCCLAAAQAVLLQPRQPPVAAAYESHEYYCEPQAQPKAHASKDLEEQLR 60

Qy 61 SVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNSERAKLTSFLKDALTAEKMSVNAKGSL 120
Db 61 SVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNSERAKLTSFLKDALTAEKMSVNAKGSL 120

Qy 121 AGKRHLSEPDTEVLTKHFVCVTDRSFYKPVSRQLKMHECIWPGCTKVYAMFGFRSQMKPH 180
Db 121 AGKRHLSEPDTEVLTKHFVCVTDRSFYKPVSRQLKMHECIWPGCTKVYAMFGFRSQMKPH 180

Qy 181 FKRTCKEHIDSVTSLVNNIECQICCDKKLDIVTKQHEIFKDSHNTAYSIRIPTLRNCNMT 240
Db 181 FKRTCKEHIDSVTSLVNNIECQICCDKKLDIVTKQHEIFKDSHNTAYSIRIPTLRNCNMT 240

Qy 241 TCPKNHVWNNQIWVRCKLYQNSRTCGSLRKDNGCHPLVTEYDFHGMLNLPYKYEFCPGRVK 300
Db 241 TCPKNHVWNNQIWVRCKLYQNSRTCGSLRKDNGCHPLVTEYDFHGMLNLPYKYEFCPGRVK 300

Qy 301 ISCGPNKELEVKFKSGGMDGELIYERTMLSPEVFEDLRQERIGEVKMIKAIGFLKGAAKE 360
Db 301 ISCGPNKELEVKFKSGGMDGELIYERTMLSPEVFEDLRQERIGEVKMIKAIGFLKGAAKE 360

Qy 361 GTESPNKCVELKPRHLRQDSIYRPFRCDVDICSVDPYKYAFVKFREPPEHDAYETLKHIKT 420
Db 361 GTESPAKCVELKPRHLRQDSIYRPFRCDVDICSVDPYKYAFVKFREPPEHDAYETLKHIKT 420

RESULT 2
AAW75744
ID AAW75744 standard; protein; 418 AA.
XX
AC AAW75744;
XX
DT 14-DEC-1998 (first entry)
XX
DE quail vascular endothelial growth factor-C protein.
XX
KW FLT4; vascular endothelial growth factor-C; vascular endothelial cell;
KW lymphatic endothelial cell; myelopoiesis; angiopeneses; inflammation;
KW lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS Coturnix sp.
XX
PN WO9833917-A1.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-US001973.

XX
PR 05-FEB-1997; 97US-0795430.
XX
PA (LUDW) LUDWIG INST CANCER RES.
PA (OYBE) UNIV HELSINKI LICENSING LTD.
XX
PI Alitalo K, Joukov V;
XX
DR WPI; 1998-437470/37.
DR N-PSDB; AAV52578.
XX
PT New isolated vascular endothelial growth factor polypeptide(s)
PT used to develop products for treating, e.g. cancers, inflammation,
PT oedema, granulocytopenia or for wound healing or tissue
PT transplantation
XX
PS Example 20; Page 121-124; 177pp; English.
XX
CC The vascular endothelial growth factor-C (VEGF-C) polypeptides have
CC activities affecting growth and migration of vascular endothelial cells,
CC promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC increasing vascular permeability, and affecting myelopoiesis. The
CC products can be used for stimulating angiopeneses, for inhibiting
CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC They can also be used for modulating the growth of endothelial cells.
CC They can also be used to stimulate lymphocyte production and maturation,
CC and to promote or inhibit trafficking of leucocytes between tissues and
CC lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ Sequence 416 AA;

Query Match 100.0%; Score 2354; DB 19; Length 416;
Best Local Similarity 100.0%; Prod. No. 2.8e-188;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHLLEMLSTASFCLAAGAVLLGTRQAPVAAAYESGVDYYEIEPQVGEFKAVAKSKDLEEQLR 60
Db 1 MHLTEMLSLPCCLAAAQAVLLQPRQPPVAAAYESHEYYCEPQAQPKAHASKDLEEQLR 60

Qy 61 SVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNSERAKLTSFLKDALTAAKMSVNAKGSL 120
Db 61 SVSSVDELMTVLYPEYWKMYKCQLRKGGWQHNSERAKLTSFLKDALTAEKMSVNAKGSL 120

Qy 121 AGKRHLSEPDTEVLTKHFVCVTDRSFYKPVSRQLKMHECIWPGCTKVYAMFGFRSQMKPH 180
Db 121 AGKRHLSEPDTEVLTKHFVCVTDRSFYKPVSRQLKMHECIWPGCTKVYAMFGFRSQMKPH 180

Qy 181 FKRTCKEHIDSVTSLVNNIECQICCDKKLDIVTKQHEIFKDSHNTAYSIRIPTLRNCNMT 240
Db 181 FKRTCKEHIDSVTSLVNNIECQICCDKKLDIVTKQHEIFKDSHNTAYSIRIPTLRNCNMT 240

Qy 241 TCPKNHVWNNQIWVRCKLYQNSRTCGSLRKDNGCHPLVTEYDFHGMLNLPYKYEFCPGRVK 300
Db 241 TCPKNHVWNNQIWVRCKLYQNSRTCGSLRKDNGCHPLVTEYDFHGMLNLPYKYEFCPGRVK 300

Qy 301 ISCGPNKELEVKFKSGGMDGELIYERTMLSPEVFEDLRQERIGEVKMIKAIGFLKGAAKE 360
Db 301 ISCGPNKELEVKFKSGGMDGELIYERTMLSPEVFEDLRQERIGEVKMIKAIGFLKGAAKE 360

Qy 361 GTESPNKCVELKPRHLRQDSIYRPFRCDVDICSVDPYKYAFVKFREPPEHDAYETLKHIKT 420
Db 361 GTESPAKCVELKPRHLRQDSIYRPFRCDVDICSVDPYKYAFVKFREPPEHDAYETLKHIKT 420

RESULT 3
AAW17837
ID AAW17837 standard; Protein; 419 AA.
XX
AC AAW17837;
XX

```
DT   15-JAN-1998 (first entry)
XX
DE   Human foetal liver kinase A binding protein tlk lbp.
XX
KW   Foetal liver kinase 1 binding protein; human; tlk lbp;
KW   receptor tyrosine kinase; vasculogenesis; angiogenesis;
KW   wound healing; tumour; therapy; antagonist; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig peptide
FT   Protein         21..429
FT                   /label= Mat protein
FT                   /note= "(claim 10)"
FT   Peptide         21..45
FT                   /label= N terminal
FT                   /note= "(claim 9)"
XX
PN   W-9705250-A2.
XX
PD   13-MAY-1997.
XX
PF   07-NOV-1996;   96WO-US17584.
XX
PR   08-NOV-1995;   95US-0554374.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Lyman SD;
XX
DR   WPI; 1997-281041/25.
DR   N-PSDB; AAI49811.
XX
PT   DNA encoding a human foetal liver kinase 1 binding protein    used
PT   to treat conditions with insufficient protein, deliver agents to
PT   cells and identify antagonists to treat protein mediated conditions
XX
PS   Claim 1; Page 90-92; 140pp; English.
XX
CC   This polypeptide comprises a human foetal liver kinase 1 binding
CC   protein (tlk lbp) (see AAW17837) that binds to the receptor tyrosine
CC   kinase tlk 1 expressed on vascular endothelial and tumour cells.
CC   The mature tlk1-lbp can be secreted from host cells to produce a
CC   m expression vector including an isolated tlk lbp cDNA clone (see
CC   AAW49811). Tlk lbp can be used to isolate cells which it binds,
CC   t r use in studying the roles of such cells and of tlk 1 in
CC   vasculogenesis and angiogenesis. Angiogenesis inhibition or
CC   increased vascularisation may be clinically desirable (e.g. to
CC   suppress solid tumour growth or in wound healing, respectively).
CC   The tlk-lbp can be administered to treat conditions with defective
CC   or insufficient tlk 1. Polypeptides may also act as carriers t
CC   deliver diagnostic/therapeutic agents to cells which bind;
CC   binds, to generate antibodies, and to identify tlk lig antagonists
CC   useful for treating tlk lbp mediated conditions.
XX
SQ   Sequence  419 AA;


  Query Match          75.7%;  Score 1804.5;  DB 10;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 1.6e-142;
  Matches  316;  Conservative   99;  Mismatches   0;  Indels    0;  Gaps    0;

Qy       1 MHLLEMLSLGVCLAAGAVLLSEGQ  EPVAAAYESGMGYYRRRRWVLPAAVAGVASVLILVLL 60
           |||   |:| | | | ||| | |||||   : || ||  |||  | |  |||||||||||||
Db       1 MRLIFTTSVACSLAAALIPPRQAAAAATESNLFLSTQPDNVTVLQKNDR 49

Qy      61 EVVQFVFGMGVSPLSEAYVFSTVSIAYNLTVAVLFFFMRSMHSDVWSFGILL 113
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 RSSSDDLMGVLPQVWKGPRKPWQLGPTKPGAVEFWMSLVPEVDPPTQPTRE 102

Qy     114 WEIVSLGGNPYPGIPVDANFYKLIQNGFKMDQPFYATEEIYIIMQSCWAFDS 165

RESULT   4
AAW00932
ID   AAW00932 standard; Protein; 419 AA.
XX
AC   AAW00932;
XX
DT   10-NOV-1997  (first entry)
XX
DE   Human Flt4 receptor tyrosine kinase ligand VEGF C.
XX
KW   VEGF C; Flt4; receptor tyrosine kinase; VEGFR-3; human;
KW   vascular endothelial growth factor receptor 3; ligand;
KW   angiogenesis; wound healing; lymph vessels; lymphangioma;
KW   cancer; metastasis; therapy; diagnosis; antibody; inhibitor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..102
FT                   /label= Prepro_peptide
FT   Peptide         32..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 3)"
FT   Peptide         103..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 12)"
FT   Peptide         103..224
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 13)"
FT   Peptide         103..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 11)"
FT   Peptide         115..218
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 1 )"
FT   Peptide         115..227
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 2)"
FT   Peptide         151..211
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 9)"
FT   Peptide         151..221
FT                   /note= "preferred active fragment of VEGF C,
FT                   retaining Flt4 ligand activity (Claim 8)"
XX
PN   W-9705250-A2.
XX
PD   13-FEB-1997.
XX
PF   07-AUG-1996;   96WO-FI00427.
XX
PR   28-JUN-1996;   96US-0671978.
PR   01-AUG-1996;   96US-0691334.
```

PN 12 JAN 1999; 9901 050305.
PP 14 FEB 1996; 9601 006112.
XX
PA (UYBE) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alitalo K, Joukov V;
XX
DR WPI; 1997 145008/13.
DR N-PSDB; AAI04276.
XX
PT FLT4 receptor tyrosine kinase ligand and related nucleic acid used
PT to modulate growth of endothelial cells and for diagnosis of
PT endothelial cell diseases
XX
PS Claim 7; Page 112 113; 184pp; English.
XX
CC This polypeptide comprises the pre pro sequence of human VEGF-C,
CC a novel ligand that binds specifically to human FLT4 receptor
CC tyrosine kinase (VEGFR-3), stimulating phosphorylation of the
CC receptor. Its sequence was deduced from a cDNA clone (AA104276)
CC obtd. from a PC-3 prostatic adenocarcinoma cell (ATCC CRL-1435)
CC library. The polypeptide, or its active fragments, can be
CC expressed in transformed or transfected host cells for use in
CC claimed methods for detecting endothelial cells (e.g. to mark
CC lymphatic vessels, endothelial genetics, FLT4 receptor in
CC histochemical tissue) and also to modulate the growth of mammalian
CC endothelial cells (e.g. to accelerate angiogenesis and to promote
CC endothelial function of lymphatic vessels). Inhibitors of
CC VEGF-C, such as antibodies, can be used to control endothelial
CC cell proliferation, e.g. lymphangioma or metastatic cancer.
CC Mouse and quail VEGF-C sequences (see AAW00184.1) have also been
CC isolated.
XX
SQ Sequence 419 AA;

query Match 76.7%; Score 1804.5; DB 16; Length 419;
Best Local Similarity 75.7%; Prod. No. 1.9e-142;
Matches 318; Conservative 39; Mismatches 60; Indels 3; Gaps 3;

Qy 1 MHLLEMLSLCQCVLAAGAVLLGARLQ-EPVAAAYESGDLYYEEEPDAGARKAHAFYEELA 59
Db 1 mhllqttlszacslfaaallpppreapaaaatesqldlsdaepdaqeaatayaskdleeql 60

Qy 60 RSVSSVDELMTVLYPEYWKMEKCQLRKGGWQHNREEANLNSRTEETIKFAAAHYNAEILK 119
Db 61 rsvsssvdelmtvlypeywkmykcqlrkgqwqhnrqeanlnsrteetikfaahyntdiik 120

Qy 120 SIDIEWKKIQPKMPREVVVDLGKEEKGATLNTFEKRFSVSIYRQDQGNCASPGMNISINY 179
Db 121 sidsewkkpqmpqrevvidlgkeekgatlntfekrfsvsiyrqdqgncasqpgmnisiny 180

Qy 180 TSKELEEITVPLSIRGPKPVIVSFANHTSCPCMSKLDVYKQVHSIIRRSLPATLPQCHVAN 239
Db 181 tskllqeitvplsiqppkpvtistanhtscpcmskldvyrqvhsiirrslpatlpqcpqan 240

Qy 240 KTCPTKNHVWNNGTICKCKLAHHGPGESSHLGDSDIFSSVFH IGPNKELLDEIQLVTKSV 299
Db 241 ktcptnywwnnhierclacpedtmtssdapd dstdqtthdiqpnkeldeetqepgsrtapl 299

Qy 300 RDISQLGIHKELLEKAESQQGMCKNKLLDSSQGPNKEPDEIKKQVVSKETVKKDNKNAKL 359
Db 300 rpasqphkeldrnsepgvskaklfpsqpqanretdentqpgvskllqnqpipdpkesa 359

Qy 360 CEGLEGPNKCTLKCKKFHHGQTCSQYYRPGCIVRTKRCDAGFLLAEEVCECVEVSACPKDN 419
Db 360 cestesgpkclikkkthhqtcsqyyrpgcivrtkrcdagfllaeevcecveisacpkdn 419

RESULT 5
AAW75716
LV AAW75716 standard; protein; 419 AA.
XX
AC AAW75716;
XX
DT 20-NOV-1998 (first entry)
XX
DE Human vascular endothelial growth factor C protein.
XX
KW FLT4; vascular endothelial growth factor C; vascular endothelial cell;
KW lymphatic endothelial cell; myelopoiesis; antiodemesis; inflammation;
KW lymphangiogenesis; oedema; elephantiasis; Milroy's disease.
XX
OS Homo sapiens.
XX
PN WO9833917-A1.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-US001973.
XX
PR 05-FEB-1997; 97US-0795430.
XX
PA (LIBA-) LUDWIG INST CANCER RES.
PA (UYBE-) UNIV HELSINKI LICENSING LTD.
XX
PI Alitalo K, Joukov V;
XX
DR WPI; 1998-434179/37.
DR N-PSDB; AAV52676.
XX
PT New isolated vascular endothelial growth factor polypeptide(s)
PT used to develop products for treating e.g. cancers, inflammation,
PT oedema, granulocytopenia or for wound healing or tissue
PT transplantation
XX
PS Claim 1; Page 112 115; 177pp; English.
XX
CC The vascular endothelial growth factor C (VEGF-C) polypeptides have
CC activities affecting growth and migration of vascular endothelial cells,
CC promoting growth of lymphatic endothelial cells and lymphatic vessels,
CC increasing vascular permeability, and affecting myelopoiesis. The
CC products can be used for stimulating angiogenesis, for inhibiting
CC angiogenesis, for stimulating lymphangiogenesis, treatment or prevention
CC of inflammation, oedema, elephantiasis, or Milroy's disease. They can
CC also be used to modulate myelopoiesis, e.g. treating granulocytopenia.
CC They can also be used for modulating the growth of endothelial cells.
CC They can also be used to stimulate lymphocyte production and maturation,
CC and to promote or inhibit trafficking of leucocytes between tissues and
CC lymphatic vessels or to affect migration in and out of the thymus.
XX
SQ Sequence 419 AA;

query Match 76.7%; Score 1804.5; DB 19; Length 419;
Best Local Similarity 75.7%; Prod. No. 1.9e-142;
Matches 318; Conservative 39; Mismatches 60; Indels 3; Gaps 3;

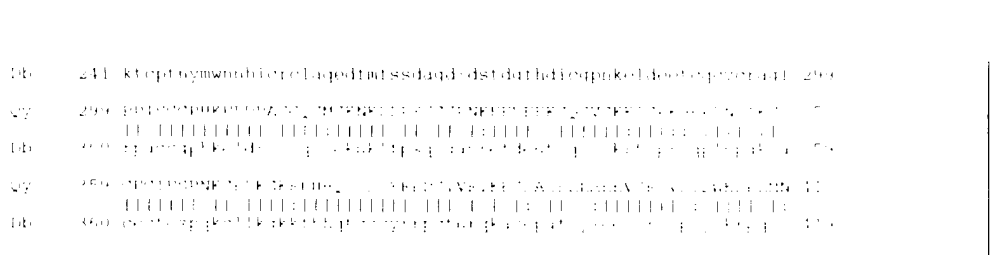
Qy 1 MHLLEMLSLCQCVLAAGAVLLGARLQ-EPVAAAYESGDLYYEEEPDAGARKAHAFYEELA 59
Db 1 mhllqttlszacslfaaallpppreapaaaatesqldlsdaepdaqeaatayaskdleeql 60

Qy 60 RSVSSVDELMTVLYPEYWKMEKCQLRKGGWQHNREEANLNSRTEETIKFAAAHYNAEILK 119
Db 61 rsvsssvdelmtvlypeywkmykcqlrkgqwqhnrqeanlnsrteetikfaahyntdiik 120

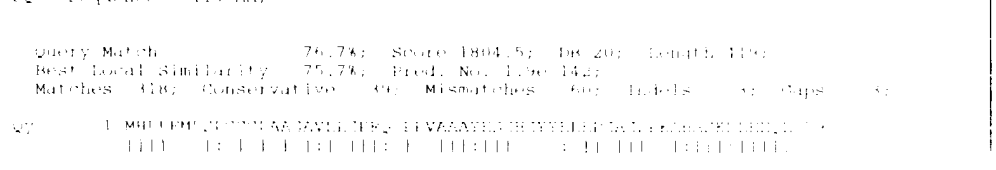
Qy 120 SIDIEWKKIQPKMPREVVVDLGKEEKGATLNTFEKRFSVSIYRQDQGNCASPGMNISINY 179
Db 121 sidsewkkpqmpqrevvidlgkeekgatlntfekrfsvsiyrqdqgncasqpgmnisiny 180

Qy 180 TSKELEEITVPLSIRGPKPVIVSFANHTSCPCMSKLDVYKQVHSIIRRSLPATLPQCHVAN 239
Db 181 tskllqeitvplsiqppkpvtistanhtscpcmskldvyrqvhsiirrslpatlpqcpqan 240

Qy 240 KTCPTKNHVWNNGTICKCKLAHHGPGESSHLGDSDIFSSVFH IGPNKELLDEIQLVTKSV 299



RESULT 6
AAW86203
ID AAW86203 standard; protein; 419 AA.
XX
AC AAW86203;
XX
DT 15-FEB-1999 (first entry)
XX
DE Human vascular endothelial growth factor (VEGF) C sequence.
XX
KW VEGF; VRP; vascular endothelial growth factor; VEGF-related protein;
KW recombinant; truncated; gene therapy; antiangiogenic; cardiovascular;
KW coronary; collateral vessel development; cell growth; migration; heart;
KW lower limb ischaemia; stroke; peripheral vascular disease; wound healing;
KW wound healing; skin; vascular permeability.
XX
OS Homo sapiens.
XX
PN WO9819300-A2.
XX
PD 07-MAY-1998.
XX
PF 20-APR-1998; 98WO-US007801.
XX
PR 25-APR-1997; 97US-0842984.
XX
PA (CHUG-) COLLATERAL THERAPEUTICS.
XX
PI Bohlen P;
XX
DR WPI; 1998-289426/01.
XX
PT New truncated vascular endothelial growth factor related protein
PT subunits - lack part of the N terminal sequence, used to stimulate
PT angiogenesis, e.g. for treating heart disease and ischaemia
XX
PS Disclosure; Fig 1; 113pp; English.
XX
CC This represents the amino acid sequence of human vascular endothelial
CC growth factor (VEGF)-C protein. The invention provides truncated VRP
CC (VEGF-related protein) subunits that have at least one amino acid
CC N terminal to the first Cys of the core sequence deleted. Host cells
CC transformed or transfected with expression vectors containing nucleic
CC acids encoding the truncated VRP subunits are used to produce the
CC truncated proteins recombinantly. The truncated VRP subunits, optionally
CC expressed from gene therapy vectors, have in vivo and in vitro angiogenic
CC activity and are used to stimulate angiogenesis, particularly coronary
CC collateral vessel development in cases of cardiac ischaemia; to stimulate
CC endothelial cell growth and migration in vitro; to treat heart disease;
CC to treat ischaemia (e.g. cardiac, chronic coronary or chronic lower limb
CC ischaemia; stroke and peripheral vascular disease); to promote healing of
CC wounds (of skin or intestines), and to increase vascular permeability.
XX
SQ Sequence 419 AA;



RESULT 7
AAB10648
ID AAB10648 standard; Protein; 419 AA.
XX
AC AAB10648;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair, wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; VEGF.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US030503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164113.
XX
PA (JANS-) JANSSEN PHARM NV.
XX
PI Gordon RD, Spronnel JJ, Yon JK, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds
XX
PS Disclosure; Fig 11; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularisation.

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CC   regulator. An antisense molecule of the invention is useful for treating
CC   or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC   retinopathy by inhibiting angiogenic activity or inappropriate
CC   vascularization including formation and proliferation of new blood
CC   vessels. Growth and development of tissues, tissue regeneration and wound
CC   and tissue repair in a subject. The products of the invention are useful
CC   for preparing medicaments for treating wounds such as dermal ulcers,
CC   pressure sores, venous sores, diabetic ulcers and burns, and to promote
CC   skin graft growth, tissue repair, proliferation of new blood vessels,
CC   tissue regeneration and organ repair by promoting angiogenic activity or
CC   vascularization. This sequence represents the human VEGF protein used
CC   to illustrate the method of the invention.
XX
SQ   Sequence   419 AA;


  Query Match             76.7%;  Score 1804.5;  DB 21;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-142;
  Matches  418;  Conservative   39;  Mismatches   60;  Indels    5;  Gaps    5;

Qy       1 MHLLEMLSLGLCLAAGAVLLGPGQ PPVAAAYESGDLYYEEFQGAGEPKAHASKLDEEQL 59
           ||||   ||| | | | ||| | |||| |  |||:|||    : || |||   | ||| |||
Db       1 mhlhtttszacsllaaallpapresapaaaaatesqhdlsdaepdaeatatayaskdleeql 60

Qy      60 RSVSSVLHELMVLVTPEYWKMDKTVLPKQCWLHNEIGFGSGQFAVVKKCQWLNKQTAVKIIK 119
           |||||||||||||||||||||||||||||||| :: ::|:::::|||||||| |||
Db      61 rsvssvdelmtvlypeywkmykspihkpgswlhnrdvgfgsgqfavvkkcpwlnkqtavkiik 120

Qy     120 SHFQEWRKLQMMPREVQVVLQKEDPGATLNIIFKDEVSTYPDFTCSGTQVNESIGLQMNLSNY 179
           ||| |||||| |||||||:|||||  |||||||||||:|||||||| |||| |||
Db     121 srdheqlkkdfmpeaqvlqkldhpnvvklvatatlkkpevsvyreqlelnpnnsvlqemnqlsvy 180

Qy     180 LSKILLEELVPLSHPGPKPVIVSFANDISCPCMSKLLVYHLVIELIRRDSLPAIGLQCHVAN 239
           :|||||||||||| |||||:|||||||||||||||||||||||||||||||||  || |
Db     181 lskfleeitvplshpgpkpvlisfanditscpcmskltvyhgvielirrdslpaiglqchvan 240

Qy     240 KLCPKNHVWNNGLTSCLAGRDFSSHLDSGDFIFGTFDTRPNKFLEEFQVCKGV 293
           |||| |:||| ||||||| || ||| || |:::||| |||||||||||||||| |
Db     241 klcptqymwnnhirclaqedfmtssdaepf dstdqfhdficqpnkcldeetcpcvcnal 299

Qy     294 PFIQTTHKEILRAIQPWCPLENKEREYCLQGGKMVTKLICPKHDCLNFAVCL 345
           | ||||:|||| |||||:||| || || |:|||  ||||||:|||| |||| |
Db     300 pqasqphkcldnsaqpcvcnklfpspqsmnctdeatepcvckttcpsgqpprdrgdpnykfg 359

Qy     346 GKWTHEINGKTFEKGKKFEMDLFSGTLAYEFVLEEPTAEMVRERLAHIVVTDYMEDMYFW 405
           .|||||| || |||||:|||||||| ||| | | | |:  :|||||| | |||| ||
Db     360 gqetcspqpkellkpggtfqlgtcevvpgnpkqvqpatfgsvgaitltyktflpndygfkik 419

RESULT   8
AAK20048
ID   AAK20048 standard; Protein; 419 AA.
XX
AC   AAK20048;
XX
DT   01-JAN-2001  (first entry)
XX
DE   Human VEGF-C protein sequence.
XX
KW   Human; FLT4; tms like tyrosine kinase 4; lymphoedema;
KW   vascular endothelial growth factor receptor 3; VEGFR-3;
KW   Milroy Nonne syndrome; lymphoedema praecox; VEGF-C;
KW   vascular endothelial growth factor C.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A1.
XX
PD   05-OCT-2000.
XX
PF   29-MAR-1999;   99WO-US006143.
XX
PR   29-MAR-1999;   99WO-US006143.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
PA   (HELS-N) UNIV HELSINKI LICENSING LTD OY.
PA   (HAYF ) UNIV HELSINKI.
XX
PI   Ferrell RE, Alitalo K, Finegold DN, Kaikkonen M;
XX
DR   WPI; 2000-679298/65.
DR   N-PSDB; AAK20406.
XX
PT   Screening a human subject for increased risk of developing a lymphatic
PT   disorder, comprises assaying a nucleic acid to determine a mutation
PT   affecting the sequence of a vascular endothelial growth factor
PT   receptor-3.
XX
PS   Disclosure; Page 64; 76pp; English.
XX
CC   The present sequence is the protein sequence for the human vascular
CC   endothelial growth factor C (VEGF-C). It was used to demonstrate the
CC   methods of the invention, which involve the screening of individuals to
CC   determine which vascular endothelial growth factor receptor-3 (VEGFR-3,
CC   also known as Flt4 or tms like tyrosine kinase 4) alleles they possess
CC   and thus their likelihood of developing hereditary lymphoedema.
CC   Conditions associated with lymphoedema include Milroy Nonne syndrome,
CC   which is early onset lymphoedema and lymphoedema praecox, which is late
CC   onset.
XX
SQ   Sequence   419 AA;


  Query Match             76.7%;  Score 1804.5;  DB 21;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-142;
  Matches  418;  Conservative   39;  Mismatches   60;  Indels    5;  Gaps    5;

Qy       1 MHLLEMLSLGLCLAAGAVLLGPGQ PPVAAAYESGDLYYEEFQGAGEPKAHASKLDEEQL 59
           ||||   ||| | | | ||| | |||| |  |||:|||    : || |||   | ||| |||
Db       1 mhlhtttszacsllaaallpapresapaaaaatesqhdlsdaepdaeatatayaskdleeql 60

Qy      60 RSVSSVLHELMVLVTPEYWKMDKTVLPKQCWLHNEIGFGSGQFAVVKKCQWLNKQTAVKIIK 119
           |||||||||||||||||||||||||||||||| :: ::|:::::|||||||| |||
Db      61 rsvssvdelmtvlypeywkmykspihkpgswlhnrdvgfgsgqfavvkkcpwlnkqtavkiik 120

Qy     120 SHFQEWRKLQMMPREVQVVLQKEDPGATLNIIFKDEVSTYPDFTCSGTQVNESIGLQMNLSNY 179
           ||| |||||| |||||||:|||||  |||||||||||:|||||||| |||| |||
Db     121 srdheqlkkdfmpeaqvlqkldhpnvvklvatatlkkpevsvyreqlelnpnnsvlqemnqlsvy 180

Qy     180 LSKILLEELVPLSHPGPKPVIVSFANDISCPCMSKLLVYHLVIELIRRDSLPAIGLQCHVAN 239
           :|||||||||||| |||||:|||||||||||||||||||||||||||||||||  || |
Db     181 lskfleeitvplshpgpkpvlisfanditscpcmskltvyhgvielirrdslpaiglqchvan 240

Qy     240 KLCPKNHVWNNGLTSCLAGRDFSSHLDSGDFIFGTFDTRPNKFLEEFQVCKGV 293
           |||| |:||| ||||||| || ||| || |:::||| |||||||||||||||| |
Db     241 klcptqymwnnhirclaqedfmtssdaepf dstdqfhdficqpnkcldeetcpcvcnal 299

Qy     294 PFIQTTHKEILRAIQPWCPLENKEREYCLQGGKMVTKLICPKHDCLNFAVCL 345
           | ||||:|||| |||||:||| || || |:|||  ||||||:|||| |||| |
Db     300 pqasqphkcldnsaqpcvcnklfpspqsmnctdeatepcvckttcpsgqpprdrgdpnykfg 359

Qy     346 GKWTHEINGKTFEKGKKFEMDLFSGTLAYEFVLEEPTAEMVRERLAHIVVTDYMEDMYFW 405
           .|||||| || |||||:|||||||| ||| | | | |:  :|||||| | |||| ||
Db     360 gqetcspqpkellkpggtfqlgtcevvpgnpkqvqpatfgsvgaitltyktflpndygfkik 419

RESULT   9
AAY20419
ID   AAY20419 standard; Protein; 419 AA.
XX
AC   AAY20419;
XX
DT   17-AUG-2000  (first entry)
XX
DE   Human prepro vascular endothelial growth factor C.
XX
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```
KW   human; receptor tyrosine kinase; RTK; Flt1; tms like tyrosine kinase 1;
KW   VEGFR 1; vascular endothelial growth factor receptor 1; thrombospondin;
KW   cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW   neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW   sarcoma; malignancy; VEGF C; vascular endothelial growth factor c.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= signal-peptide
FT   Peptide         32..108
FT                   /label= N-terminal peptide
FT                   /note= "cleavage of this peptide is a prerequisite for secret
FT                   VEGFR-1 produces a fully processed mature form of VEGFR-1
FT                   of 21-23 kD which has high affinity to VEGF-A"
FT   Protein         1..227
FT                   /label= Mature VEGFR-1
FT   Peptide         228..419
FT                   /label= C-terminal peptide
FT                   /note= "Has a pattern of spaced cysteine residues
FT                   reminiscent of a Balbiani ring protein (BRP) sequence;
FT                   cleavage of signal peptide and the C-terminal
FT                   peptide produces a partially processed form of VEGFR-1 of
FT                   about 29 kD which has high affinity to Flt1 (VEGFR-1)"
FT   Binding-site    114..214
FT                   /note= "Ig-like subclass V-2 domain of..."
FT                   at position 156 is essential for VEGFR-2 binding and at
FT                   165 is essential for VEGFR-2 and VEGFR-1 binding"
FT   Region          131..211
FT                   /note= "Ig-like subclass V-2 domain"
XX
RN   [1]
RP   1-419
RX   WO200218586-A1.
XX
RD   28-FEB-2002.
XX
RP   1-419
RX   DOI; 10.2903/j.efsa.2009.1141.
XX
PA   (SUGA-) SUGANO GENE RES CENTRE KK.
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI   Alitalo K, Kaipainen A, Valtola R, Jussila L;
XX
DR   WPI; 2002-317865/34.
XX
PT   Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
PT   and sarcomas, involves administering a compound capable of inhibiting
PT   binding of ligand proteins to tms like tyrosine kinase 4 receptor
XX
PS   Example 15-17; Page 140-142; 148pp; English.
XX
CC   The patent discloses a method to treat neoplastic disease characterised
CC   by expression of tms like tyrosine kinase 4 (Flt4) receptor (also
CC   referred as vascular endothelial growth factor receptor 3, VEGFR-3) in
CC   endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC   method involves administering a compound that inhibits ligand-a
CC   ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC   endothelial cells. The compound is useful for treating neoplastic disease
CC   such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC   and sarcomas. Flt4 receptor tyrosine kinase binding ligands can be used
CC   in a manufacturing medicament useful for diagnostic screening, imaging and
CC   treatment of malignancies characterised by Flt4 expressing blood cells.
CC   The Flt4 gene maps to chromosomal region 5q35 and is expressed as 5.8 kb
CC   and 4.5 kb mRNAs which differ in their 3' sequences and are
CC   differentially expressed in HEL and DAMI cell lines. Flt4
CC   belongs to a subfamily of class III receptor tyrosine kinases (RTKs).
CC   It is used as a target for tumour imaging and anti tumour therapy.
CC   The present sequence is a human prepro vascular endothelial growth
CC   factor C (VEGF-C), a specific example of Flt4 binding ligand.
XX
SQ   Sequence   419 AA;
```

```
  Query Match             76.7%;  Score 1804.5;  DB 21;  Length 419;
  Best Local Similarity   75.2%;  Pred. No. 1.9e-142;
  Matches  318;  Conservative   99;  Mismatches   60;  Indels    5;  Gaps    5;

Qy       1 MHLLEMLSLGQCTLAACAVLLCFPV PVVAAAYESGHGYYEEEPQAGEIKAHASKPLEEQL 60
           |||   |: | | | |:| ||| | |||:||    : :| ||| :: |:|:|:|
Db       1 mhlliflsasfsllaaalfapqpreqpaaaaatesaldlsdaepdagealqyaskdleeql 60

Qy      61 RSVLLVDTKDAERSVRQLGDNAELELKTLVEAQSNAEFQKEIL 102
           |||||||||||| |||||||||:|||:|||||||| :: :|||:::|||'|||| |||
Db      61 rsvssvdtaeaslypqqvkmyplrvqlkstmdshsilqnlrnqdkl 106

Qy     103 PTPTEWRKTQCMPREVDVDLGDEFDAQLNTTFPLMVDFQNWSARSTKLAESLQHMDEQFKS 162
           ||| ||||P| |:|||||:|||||  |||||||||||:|||:|||||||||| ||:|:
Db     107 sidnewrktpqmprrsidqakdvlttlkppdesvyvqdrvkseiqgtngnsvdlpmqlksv 166

Qy     163 LSKLLFPIVPLSRLQKPVIVSIANDLSCMSSELVYFQVRSLTGGSDEPAIGLQPMVAN 220
           :|||||||||||| |||||:|||||||||||||||||||||||||||||||||||  ||  ||
Db     167 lskllqlvypisppqkpqtistnqhtsqcmsskldvyqrtslirlspatppppaan 224

Qy     221 KTCPKNHVWNNQLTACHELGGNSHLVDNSDLVEDFISDRKRLEDIEKLIGMGGV 274
           |||| |:|||| ||||||| || |||  || |:|:|||| ||||||||||||||||| ||
Db     225 ktcptqymwnnhlvrclaqeddntdssdaad dstdafhdicapnkeldeetqvqvtaal 280

Qy     275 RSSSGLKDDPNLSLLKNLSTIDHIKAQRAAEQANDLENLILDLEKKHSSLQENVFSAKEA 334
           |||| |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     281 rpsqqpkkcdpsfqsqpwnhkdlpsptarscqdeqaqvqgtgvgdsetwrkpvfiengaha 340

Qy     335 VEKSVQAVEKGQVILAVDEKNPKELVVLDLEDMPLTTHFSLQSLVDMALGEIQSRLEDVR 394
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 vekstvqavekgqvilavdeknpkelvvldledmpltthfslqslvdmalgeiqsrledvr 400

Qy     395 SLMGQVSMELEPCLGHCNTTVHNLIKNVKDQMDKDLSNKMDMQNKV 439
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     401 slmgqvsmelepclghcnttvhnlikdvkdqmdkdlsnkmdmqnkv 445


RESULT  10
AAY70982
ID   AAY70982 standard; protein; 419 AA.
XX
AC   AAY70982;
XX
DT   09-AUG-2000  (first entry)
XX
DE   Human vascular endothelial growth factor (VEGF)-C protein.
XX
KW   Vascular endothelial growth factor C; VEGF; human; tumour; endothelial cell;
KW   vascular endothelial growth factor receptor; VEGFR; vascular trauma;
KW   blood vessel; cardiovascular surgery; anti restenosis agent; prevention;
KW   restenosis; stenosis; percutaneous transluminal coronary angioplasty.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..31
FT                   /label= Signal peptide
FT                   /note= "cleavage results in partially processed VEGF-C
FT                   protein (29 kD)"
FT   Peptide         32..108
FT                   /label= Amino terminal peptide
FT                   /note= "cleavage results in fully processed mature
FT                   VEGF-C protein (21-23 kD)"
FT   Protein         109..227
FT                   /label= Mature human VEGF-C
FT                   /note= "processed vascular epithelial growth factor-C"
FT   Binding-site    83
FT                   /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT   Active site     131..211
FT                   /note= "Essential for biological activity of protein"
FT   Binding site    137
FT                   /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT   Binding site    156
FT                   /note= "Essential for VEGFR-2 binding"
FT   Binding site    165
```

```
FT                     /note= "Essential for VEGFR-2 and VEGFR-3 binding"
FT   Peptide           228..419
FT                     /label= Carboxy terminal peptide
FT                     /note= "Cleavage results in partially processed VEGF-C
FT                     protein (29 kD)"
XX
PN   WO2000044772-A2.
XX
PD   04-MAY-2000.
XX
PF   26-OCT-1999;    99WO-US025054.
XX
PR   26-OCT-1998;    98US-0105907
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD OY.
PA   (YLAH/) YLA-HERTTUALA S.
XX
IN   Ylae-Herttuala S;  Alitalo K;  Riittinen M-L;  Jeltsch MM;  Achen MG;
XX
DR   WPI; 2000-356564/30.
DR   N-PSDB; AAB00839, AAB00853.
XX
PT   Preventing stenosis and restenosis in mammals using vascular
PT   endothelial growth factor proteins or the nucleic acid encoding them
XX
PS   Claim 5; Page 51-54; 94pp; English.
XX
CC   The present amino acid sequence is the complete human prepro vascular
CC   endothelial growth factor (VEGF) C. VEGF-C has the ability to stimulate
CC   re-endothelialisation of an injured blood vessel, without significant
CC   stimulation of smooth muscle cell proliferation. It can bind to and
CC   stimulate VEGFR-2 (vascular endothelial growth factor receptor) and/or
CC   VEGFR-3 phosphorylation in cells that express such receptors. An
CC   anti-restenosis agent comprising either a VEGF-C gene or protein is
CC   used in a method to reduce or prevent restenosis and stenosis of a blood
CC   vessel following vascular trauma (e.g., cardiovascular surgery and
CC   percutaneous transluminal coronary angioplasty.
XX
SQ   Sequence  419 AA;


  Query Match             76.7%;  Score 1804.5;  DB 21;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-142;
  Matches  418;  Conservative   39;  Mismatches   60;  Indels    3;  Gaps    3;

Qy       1 MHLLGFGLSLGCYAAVLELDNVLSVVANDLPTVAAAYFSGIGYYFEWKSFDLRLAHASKIEERGL 64
           ||||   ||:|| | | | |:|| |||:| |  |||:|||     : || |||  |:|||||||||
Db       1 mhllqftsvacslllaallpgpttaapaaaaatesqldlsdaepdaqeatqvcsgkdlevqlkdlee 64

Qy      65 RSVSSVLHELMTVLYFEYWKMFKCQLRKCGWQHNEIGTSYRSVIRIDIGLKFAAAHYNAFIFK 129
           ||||||||||||||||||||||||||||||| :: :|:|:::::|||||||| ||||
Db      65 rsvssvldelmtvlypeywkmykcqlrkcgwqhneigtsyrsviririgvefaaahynafifk 129

Qy     130 SIDIEWRKTQPGMDRDEVCVDLCKEFGALENITEKKPPVSIYWCGPGNSIGNLTHVCVQNGCNK 193
           ||| ||||||:|||||||:|:|||||  |||||||||||||:|||||||||| | | | ||||
Db     129 saihewrktqpgmdrdevcvdlckefgalenitekkppvsiywcgpgnsignltHVCVQNGCNK 193

Qy     194 ISKTLEEFLTVFSLDRYNLGDCIPCMCKLDVYRQVHSIIRRSLPATLPQCQAVNKTCPTNYAN 257
           :|||||||||||||| ||||||:|||||||||||||||||||||||||||||||||| ||  ||
Db     194 lskilkefltvfslprpnlgdcipcmckldvyrqvhsiirrslpatlpqcqavnktcptnyan 257

Qy     258 KLKFKNHVWNNQVFVLAGLMHDGIPCNITGDDISSCEHRGNKLLSDLVFVLEKSTQFMTLQPE 321
           |||| |:|||| |||||| || ||:|:|:|||:|||||:|||||:|:|:|:|:|:|:|:|:|:
Db     258 klkfqnhvwnnhiverhepedtmtssstaqvdstdqthatvqptnkeddevhvepvyfnkskfn 321

Qy     322 PKPLSGRQLALIAGVVVGVVLLLVIVVGVLFWHLRKRTQKAKQMSFEYQSSVHLTSFKNSSVE 385
           |  |:|:|:|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     322 passpqtqkeldnnsepvzekvnkiipspeqnnretdentepvzektqetnqpqlqpnpkhvp 385

Qy     386 GSYLEGSNKCILKGKEFHIQIGSCYPDCTVKTKKCMAGFCLAEEVCECVELWKKEGDMN 444
           |||||| |:|||:|||||||||| ||| | | |: ||  :|||||||| : |||| |:
Db     386 gsyleghnkcilkgkkfhiqiqscypdctvktkkcmagfclaeevcecvelwkkegdmn 444
```

```
RESULT  11
AAB83605
ID   AAB83605 standard; protein; 419 AA.
XX
AC   AAB83605;
XX
DT   27-FEB-2001  (first entry)
XX
DE   Human VEGF-C.
XX
KW   Human; gene therapy; lymphatic disorder; hereditary lymphedema; 6.54;
KW   vascular endothelial growth factor receptor 3; VEGFR 3; VEGF-C; VEGFR3;
KW   tms-like tyrosine kinase 4.
XX
OS   Homo sapiens.
XX
PN   WO200044772-A2.
XX
PD   26-SEP-2000.
XX
PF   29-SEP-1999;   99WO-US022470.
XX
PR   29-MAR-1999;   99US-0126133.
PR   16-AUG-1999;   99US-0376248.
XX
PA   (UYPI ) UNIV PITTSBURGH.
PA   (UYHE ) UNIV HELSINKI LICENSING LTD OY.
PA   (LUDW ) LUDWIG INST CANCER RES.
XX
PI   Alitalo K;  Ferrell RE;  Finegold DN;  Karkkainen M;
XX
DR   WPI; 2000-601772/57.
DR   N-PSDB; AAC68953.
XX
PT   Screening a human for an increased risk of developing lymphatic
PT   disorder, comprises assaying nucleic acid for alterations in the
PT   sequences expressing vascular endothelial growth factor receptor 3
XX
PS   Disclosure; Pages 62-63; 99pp; English.
XX
CC   The present invention relates to a method for screening a human subject
CC   for an increased risk of developing a lymphatic disorder e.g. hereditary
CC   lymphedoema. The method comprises assaying nucleic acid of a human
CC   subject to determine a presence or an absence of a mutation altering the
CC   sequence or expression of vascular endothelial growth factor receptor 3
CC   (VEGFR 3)/tms like tyrosine kinase 4 (FLT4) allele (see AAC68952 and
CC   AAB83604) and determining an increased risk of developing lymphatic
CC   disorder from presence or absence of the mutation. The presence of a
CC   mutation altering the encoded amino acid sequence or expression of at
CC   least 1 VEGFR 3 allele in the nucleic acid correlates with an increased
CC   risk of developing a lymphatic disorder. Treatment for hereditary
CC   lymphedoema can be provided through the administration of vascular
CC   endothelial growth factor C (VEGF-C) and vascular endothelial growth
CC   factor D VEGF-D genes (via gene therapy) and proteins. The present
CC   sequence is the protein sequence for VEGF-C.
XX
SQ   Sequence  419 AA;


  Query Match             76.7%;  Score 1804.5;  DB 22;  Length 419;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-142;
  Matches  418;  Conservative   39;  Mismatches   60;  Indels    3;  Gaps    3;

Qy       1 MHLLGFGLSLGCYAAVLELDNVLSVVANDLPTVAAAYFSGIGYYFEWKSFDLRLAHASKIEERGL 64
           ||||   ||:|| | | | |:|| |||:| |  |||:|||     : || |||  |:|||||||||
Db       1 mhllqftsvacslllaallpgpttaapaaaaatesqldlsdaepdaqeatqvcsgkdlevqlkdlee 64

Qy      65 RSVSSVLHELMTVLYFEYWKMFKCQLRKCGWQHNEIGTSYRSVIRIDIGLKFAAAHYNAFIFK 129
           |||||||||||||||||||||||||||||||  :: :|:|:::::|||||||| ||||
Db      65 rsvssvldelmtvlypeywkmykcqlrkcgwqhneigtsyrsviririgvefaaahynafifk 129

Qy     130 SIDIEWRKTQPGMDRDEVCVDLCKEFGALENITEKKPPVSIYWCGPGNSIGNLTHVCVQNGCNK 193
           ||| ||||||:|||||||:|:|||||  |||||||||||||:|||||||||| | | | ||||
Db     129 saihewrktqpgmdrdevcvdlckefgalenitekkppvsiywcgpgnsignltHVCVQNGCNK 193

Qy     194 ISKTLEEFLTVFSLDRYNLGDCIPCMCKLDVYRQVHSIIRRSLPATLPQCQAVNKTCPTNYAN 257
           :|||||||||||||| ||||||:|||||||||||||||||||||||||||||||||| ||  ||
Db     194 lskilkefltvfslprpnlgdcipcmckldvyrqvhsiirrslpatlpqcqavnktcptnyan 257

Qy     258 KLKFKNHVWNNQVFVLAGLMHDGIPCNITGDDISSCEHRGNKLLSDLVFVLEKSTQFMTLQPE 321
           |||| |:|||| |||||| || ||:|:|:|||:|||||:|||||:|:|:|:|:|:|:|:|:|:
Db     258 klkfqnhvwnnhiverhepedtmtssstaqvdstdqthatvqptnkeddevhvepvyfnkskfn 321

Qy     322 PKPLSGRQLALIAGVVVGVVLLLVIVVGVLFWHLRKRTQKAKQMSFEYQSSVHLTSFKNSSVE 385
           |  |:|:|:|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     322 passpqtqkeldnnsepvzekvnkiipspeqnnretdentepvzektqetnqpqlqpnpkhvp 385

Qy     386 GSYLEGSNKCILKGKEFHIQIGSCYPDCTVKTKKCMAGFCLAEEVCECVELWKKEGDMN 444
           |||||| |:|||:|||||||||| ||| | | |: ||  :|||||||| : |||| |:
Db     386 gsyleghnkcilkgkkfhiqiqscypdctvktkkcmagfclaeevcecvelwkkegdmn 444
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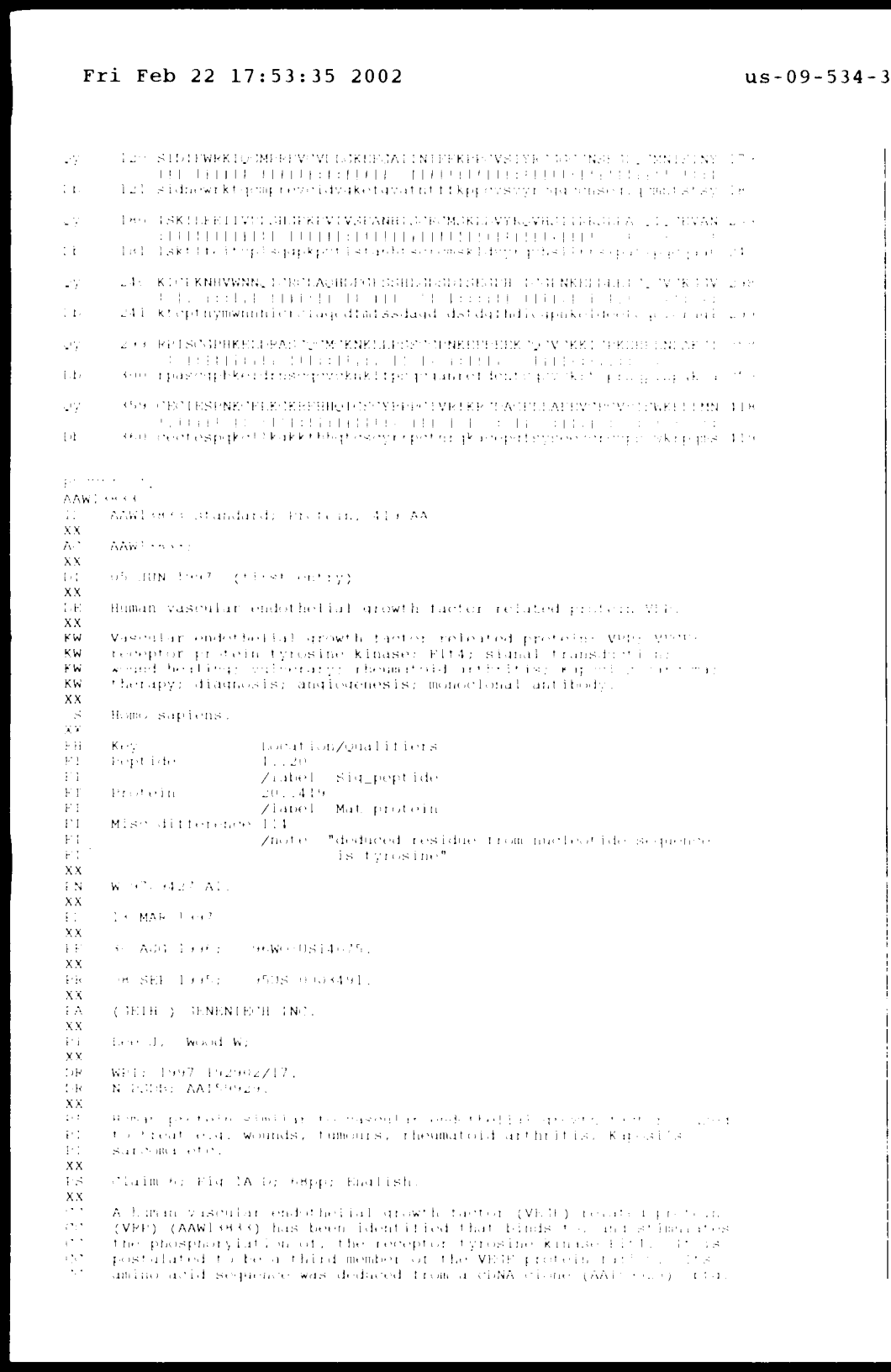

AAW18033
AAW18033 standard; Protein; 419 AA.
XX
AC AAW18033;
XX
DT 05-JUN-1997 (first entry)
XX
DE Human vascular endothelial growth factor related protein, VRP.
XX
KW Vascular endothelial growth factor related protein; VRP; VEGF;
KW receptor protein tyrosine kinase; Flt4; signal transduction;
KW wound healing; inflammatory; rheumatoid arthritis; angiogenesis;
KW therapy; diagnosis; angiogenesis; monoclonal antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 20..419
FT /label= Mat protein
FT Misc-difference 114
FT /note= "deduced residue from nucleotide sequence
FT is tyrosine"
XX
PN WO9746364-A1.
XX
PD 11-DEC-1997
XX
PF 06-JUN-1997 WO-US010075.
XX
PR 06-JUN-1996 96US-0659491.
XX
PA (GETH-) GENENTECH INC.
XX
PI Lee J, Wood W;
XX
DR WPI; 1997-592002/17.
DR N-PSDB; AAI59029.
XX
PT Human protein similar to vascular endothelial growth factor - used
PT to treat ocular wounds, tumours, rheumatoid arthritis, Kaposi's
PT sarcoma etc.
XX
PS Claim 6; Fig 2A-D; 98pp; English.
XX
CC A human vascular endothelial growth factor (VEGF) receptor protein
CC (VRP) (AAW18033) has been identified that binds to, and stimulates
CC the phosphorylation of, the receptor tyrosine kinase Flt4. It is
CC postulated to be a third member of the VEGF protein family. The
CC amino acid sequence was deduced from a cDNA clone (AAI59029). The
CC protein is useful for stimulating angiogenesis and lymphangiogenesis
CC in vitro and in vivo. It is also useful for screening for
CC antagonists and agonists which may be used to treat conditions
CC associated with abnormal angiogenesis, lymphangiogenesis or vascular
CC permeability. The protein may also be used to raise monoclonal
CC antibodies which may be used to treat conditions associated with
CC abnormal angiogenesis or vascular permeability. VRP may make it
CC possible to avoid coronary bypass surgery by stimulating growth of
CC the collateral circulation.
XX
SQ Sequence 419 AA;

Query Match 29.5%; Score 1295.5; DB 18; Length 419;
Best Local Similarity 25.7%; Pred. No. 1.1e-141;
Matches 317; Conservative 80; Mismatches 61; Indels 37; Gaps 3;

Qy 1 MHLLEMLSLAVVLAACAVLLCPAQ-EPVAAAAYESGDYYEEEPQACEPKAHASKDLEEQL 59
|||| :: | | | :: :| :: | |:|:|| : :| ||| ||:|:|||:|
Db 1 mhllqttsvacslladlpapqpreapaaaafesqvdlsdaepdhvtetayayaskdleeql 60

Qy 60 SLVSATDLMDLAVLVTEWEMDEADHDYEDQHSEIEKRLASLGKLSDKVLRFEAAAADNAPLEP 119
||||||| | |:|||||:|:|| |||||||| :: ||||||||:|:| | |||
Db 61 rsvssvqdmtvlypeyvkaqvgkpkqagvepqrlfqqvwpherrqpaplqsfaaeftmrirdvdgtgrsaylkg 120

Qy 120 SIDIEWKKIEVVDEQGKDSVFYGTLNKLKVEKCGCIA-NLTESYGVTECTMRGVCHFSRYP 178
||| |||||| |||| |:|:|||:| |||||||||||:|:|||||||||||||||||:|| ||
Db 121 sidnewrktqvvwkeegkevatlatlikpevsvyteqqrcnsgglpddaqcltkggevssfhtrktfsfrrpr 180

Qy 179 PKPESSGVCGSLRAASVTLDQSRVNLTCSETQNHPLKMTQVTFLLKLGKEDWKLERLSFTEQ 238
||||||||||||| |||||:|||||||||||||||||||||||||||||||||||||||||| ||
Db 181 pkpetgtvcpslpdyeptfstvdvpltvevfhpkvtsfmelevkpkvtvewlkdgvpmetkvlhpsktkftmp 240

Qy 239 FTVGEKLNSVWNMSIEGMVLAQLTDSYLFLMVLQHTTLQVIAYTLNTSLGPCTARNSLAPIS 298
|||| |:||| ||||||| || ||| || |:|||| |||||||||||||||||
Db 241 ktqptnymwnnhlcrclagdimasdaadnstdathdicpakeldeetqdsqcvcrtgdnqcqpgsgrvtgngh 300

Qy 299 AFHLDVSKGENLIFHATFNPRFNRHGNLIIRSTSVGRLPVVRKVDPEKHHIELMEAKSLV 358
|| |||||||||| ||||||||| || || |:|||| |||||||:|||| |||| ||
Db 301 rpasqahkqldmssqpnqtkntpsptarnrldaqtgeevpkttqvrpdqhcrtqvegsyrcltdnyiqkepk 360

Qy 359 CEGIESPNGCFEVGRFHHQHCVSTYFHVCVPLKMAGTLLAEFVGWSWKPFQLMNKIWAKVN 418
|||||| || ||||:|||||||||| || | | |: || :|||||| | |||| ::
Db 361 ceetospqhqfiksklpvqvsvrpdtrqkvcopafsysnnrcsfpeqkvcesvtgwkpqdsmpwkfvgldps 419

RESULT 13
AAY30518
AAY30518 standard; Protein; 419 AA.
XX
AC AAY30518;
XX
DT 19-NOV-1999 (first entry)
XX
DE Vascular endothelial growth factor-2 (VEGF-2).
XX
KW Human vascular endothelial growth factor-2; VEGF-2;
KW vascular endothelial cell growth; endothelial cell migration;
KW angiogenesis; blood pressure; blood flow; immune system disorder;
KW immune cell; cancer; autoimmune disorder; blood protein disorder;
KW ataxia telangiectasia; common variable immunodeficiency;
KW Digeorge syndrome; HIV infection; HTLV-BLV infection;
KW leukocyte adhesion deficiency syndrome; lymphopenia;
KW phagocyte bactericidal dysfunction; severe combined immunodeficiency;
KW Wiskott-Aldrich disorder; anemia; thrombocytopenia; hemorrhoids;
KW allergy; asthma; allergic asthma.
XX
OS Homo sapiens.
XX
PN WO9946364-A1.
XX
PD 16-SEP-1999.
XX

RESULT 11
AAY22320
ID AAY22320 standard; Protein; 419 AA.
XX
AC AAY22320;
XX
DT 22-SEP-1999 (first entry)
XX
DE Full length human VEGF2 protein sequence.
XX
KW VEGF2; vascular endothelial growth factor 2; angiogenesis; bone marrow;
KW endothelial cell proliferation; tissue damage; therapy.
XX
OS Homo sapiens.
XX
PN US5932540-A.
XX
PD 03-AUG-1999.
XX
PF 24-DEC-1997; 97US-0998811.
XX
PR 24-DEC-1996; 96US-0998811.
PR 08-MAR-1994; 94US-0207590.
PR 06-JUN-1995; 95US-0465968.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Cao L, Hu L, Rosen CA;
XX
DR WPI; 1999-441660/37.
DR N-PSDB; AAX84887.
XX
PT Vascular endothelial growth factor 2 for wound healing and vascular
PT repair
XX
PS Claim 1; Fig 1; 49pp; English.
XX
CC This sequence is the vascular endothelial growth factor 2 (VEGF2),
CC of the invention. The isolated polypeptide is useful for stimulating
CC angiogenesis, by promoting the proliferation of endothelial cells, for
CC the treatment of a wound, or for the treatment of tissue or bone disease.
XX
SQ Sequence 419 AA;

Query Match 76.2%; Score 1794.5; DB 20; Length 419;
Best Local Similarity 75.2%; Pred. No. 1.3e-141;
Matches 416; Conservative 40; Mismatches 61; Indels 4; Gaps 4;

Qy 1 MHLLEMLSLCVCLAAGAVLLQPRQ PPVAAAYESGHGYYEEEPGAGFPKAHASKDLEEQL 60
MHLLEMLSLCVCLAAGAVLLQPRQ PPVAAAYESGHGYYEEEPGAGFPKAHASKDLEEQL
Db 1 mhllemlslcvclaagavllqprq ppvaaayesghgyyeeepgagfpkahaskdleeql 60

Qy 61 RSVSSVDELMSVLVPDYWKMTKCQLPKGGWQHPEPHSSSLDFESDDSLEPAAAHYNAEIIK 120
RSVSSVDELMSVLVPDYWKMTKCQLPKGGWQHPEPHSSSLDFESDDSLEPAAAHYNAEIIK
Db 61 rsvssvdelmsvlvpdywkmtkcqlpkggwqhpephssslDfesddslepaaahynaeiik 120

Qy 121 SISIEWRKTGQMPREVCVELGKEFGALTNTPFKPCVSIYPCSGSCNSIGLQCMNTSVNY 180
SISIEWRKTGQMPREVCVELGKEFGALTNTPFKPCVSIYPCSGSCNSIGLQCMNTSVNY
Db 121 sisiewrktgqmprevcvelgkefgaltntpfkpcvsiypcsgscnsigLqcmntsvny 180

Qy 181 ISKELFEFIVPLSIPGPKPVTVSFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN 240
ISKELFEFIVPLSIPGPKPVTVSFANHTSCRCMSKLDVYRQVHSIIRRSLPATLPQCQAAN
Db 181 iskelfeivplsipgpkpvtvsfanhtscrcmskldvyrqvhsiirrslpatlpqcqaan 240

Qy 241 KTGTATGVMGSNHVRNNQASLGWFTMFLLPSNSKLQQFIDEIKKQTVCKKSTENAKQCN 300
KTGTATGVMGSNHVRNNQASLGWFTMFLLPSNSKLQQFIDEIKKQTVCKKSTENAKQCN
Db 241 ktgtatgvmgsnhvrnnqaslgwftmflLpsnskLqqfIdeIkkqtvckkstenakqcn 300

Qy 301 PTLWNGAEELDKASQVQMCKNKLLPISGGDNKGLVEPVVLKSADFLKPEIRDQYVCKTSW 360
PTLWNGAEELDKASQVQMCKNKLLPISGGDNKGLVEPVVLKSADFLKPEIRDQYVCKTSW
Db 301 ptlwngaeeldkasqvqmcknkllpisggdnkglvepvvlksadflkpeirdqyvcktsw 360

Qy 361 CTQTLSFNKCFLKSKPEHRQLVSQYRFQCIVRTKKCDAGFLLAEFVQPVKLSWKEFLMN 420
CTQTLSFNKCFLKSKPEHRQLVSQYRFQCIVRTKKCDAGFLLAEFVQPVKLSWKEFLMN
Db 361 ctqtlsfnkcflksKpehrqlvsqyrfqcivrtkkcdagfllaefvqpvklswkeflmn 420

RESULT 15
AAY67144
ID AAY67144 standard; protein; 419 AA.
XX
AC AAY67144;
XX
DT 22-DEC-2000 (first entry)
XX
DE Vascular endothelial growth factor 2 (VEGF 2).
XX
KW Vascular endothelial growth factor 2; VEGF-2; retinal angiogenesis;
KW treatment; injury; degeneration; photoreceptors; eye;
KW antivid streaks; retinitis pigmentosa; human;
KW age related macular degeneration; diabetic retinopath;
XX
OS Homo sapiens
XX
PN WO200077165-A1.
XX
PD 21-DEC-2000.
XX
PF 7-JUN-2000; 2000WO-US015947.
XX
PR 8-JUN-1999; 99US-0138178.
PR 12-JUN-1999; 99US-0138926.
PR 8-JUN-1999; 99US-0138796.
PR 22-DEC-1999; 99US-0171905.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Anderson K, Melder R, Roschke V, Rosen SM;
XX
DR WPI; 2001-553202/61.
DR N-PSDB; AAA52489.
XX
PT Treating injury or degenerati n of photoreceptors comprises
PT administering to a subject vascular endothelial growth factor 2
PT (VEGF-2)
XX
PS Claim 51; Fig 1; 252pp; English.
XX
CC Administration of vascular endothelial growth fa t r 2 (VEGF 2)
CC to a patient can be used for treating injury or degeneration
CC photoreceptors associated with e.g. antivid streaks, retinitis
CC pigmentosa, age-related macular degeneration, diabetic retinopathy.
CC The VEGF 2 promotes angiogenesis, the formation of new blood
CC vessels in the retina.
XX
SQ Sequence 419 AA;

Query Match 75.2%; Score 1764.5; DB 21; Length 419;
Best Local Similarity 75.2%; Pred. No. 1.5e-111;
Matches 316; Conservative 40; Mismatches 63; Indels 2; Gaps 2;

Search completed: February 20, 2002, 15:25:46
Job time: 315 sec